GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:01:33 ; Search time 3691.27 Seconds
(without alignments)
8940.469 Million cell updates/sec

Title: US-09-601-267-36
Perfect score: 867
Sequence: 1 agctactcaggaggctgaga.....ccctaactgagaagggcgta 867

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	110.8	12.8	466	8	AQ229478	AQ229478 HS_2021_A
	2	109.2	12.6	680	9	AG186502	AG186502 Pan trogl
	3	107.6	12.4	418	8	AQ390169	AQ390169 CITBI-E1-
	4	107.2	12.4	469	4	BM509394	BM509394 ih17f10.y
	5	107.2	12.4	516	4	BI468297	BI468297 id87b01.y
	6	107.2	12.4	529	5	BQ270800	BQ270800 ik05b06.y
	7	107.2	12.4	556	5	BQ267333	BQ267333 ik02c03.y
	8	107.2	12.4	578	7	CK825308	CK825308 ik02c03.y
	9	107.2	12.4	584	5	BU071662	BU071662 im32a11.y
	10	107.2	12.4	584	5	BU782096	BU782096 im99h05.y
	11	107.2	12.4	589	5	BQ270346	BQ270346 ik09g10.y
	12	107.2	12.4	589	5	BU783590	BU783590 in06e04.y
	13	106.8	12.3	564	5	BX507946	BX507946 DKFZp686L
	14	106.4	12.3	635	8	AQ428429	AQ428429 CITBI-E1-
c	15	106	12.2	679	6	CA428584	CA428584 UI-H-FE1-
	16	106	12.2	774	8	AQ751486	AQ751486 HS_5576_B
	17	104.8	12.1	671	8	AQ418931	AQ418931 RPCI-11-1
	18	104.6	12.1	465	8	AQ527107	AQ527107 CITBI-E1-
	19	104.6	12.1	815	5	BQ429052	BQ429052 AGENCOURT
c	20	104.4	12.0	303	4	BM672404	BM672404 UI-E-CQ0-
	21	104.4	12.0	473	8	BZ599186	BZ599186 WHACE10TF
c	22	104.4	12.0	595	5	BX099082	BX099082 BX099082
c	23	104.4	12.0	712	9	AG139751	AG139751 Pan trogl
	24	104.4	12.0	805	8	BZ604439	BZ604439 WHAAJ34TR
	25	104	12.0	516	7	CN276447	CN276447 170006001
	26	103.8	12.0	451	7	N66929	N66929 za47h09.s1
c	27	103.6	11.9	550	6	CB163810	CB163810 K-EST0224
c	28	103	11.9	837	4	BI820230	BI820230 603037070
	29	103	11.9	1074	5	BQ429712	BQ429712 AGENCOURT
c	30	102.8	11.9	318	4	BI492686	BI492686 df27g08.w
	31	102.8	11.9	340	2	AW021747	AW021747 df27g08.y
	32	102.8	11.9	608	7	CN411496	CN411496 170005322
c	33	102.8	11.9	684	9	AG109444	AG109444 Pan trogl
c	34	102.2	11.8	1614	3	CR603212	CR603212 full-leng
c	35	102	11.8	364	8	AQ333390	AQ333390 HS_5010_A
	36	102	11.8	499	6	CD694607	CD694607 EST11130
c	37	101.6	11.7	256	1	AA084337	AA084337 zn04b05.s
	38	101.2	11.7	382	1	AV764523	AV764523 AV764523
c	39	101.2	11.7	474	1	AI866580	AI866580 tz51c10.x
c	40	101.2	11.7	514	8	B37536	B37536 HS-1044-A1-
c	41	101.2	11.7	735	1	AU120382	AU120382 AU120382
	42	101.2	11.7	773	4	BG221771	BG221771 RST41586
	43	101.2	11.7	815	2	BF382750	BF382750 601816513
c	44	101.2	11.7	859	8	AQ750588	AQ750588 HS_5573_B
	45	101.2	11.7	867	5	BU853592	BU853592 AGENCOURT

ALIGNMENTS

RESULT 1
AQ229478/c
LOCUS AQ229478 466 bp DNA linear GSS 26-SEP-1998
DEFINITION HS_2021_A2_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2021 Col=16 Row=A, genomic survey sequence.
ACCESSION AQ229478
VERSION AQ229478.1 GI:3654707
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 466)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2021 row: A column: 16
Class: BAC ends
High quality sequence stop: 466.
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source 1. .466
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2021 Col=16 Row=A"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
ORIGIN

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Best Local Similarity 90.8%; Pred. No. 5.6e-17;

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  Matches  118;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||||||||||||||| || ||||||| |||||||| |||||| ||||||||||||
Db        399 AGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAGGCGGAGGTTGCAGTG 340

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||| |||||||||||| |  |||||||||||| |||| || ||||||||||||||||||
Db        339 AGCCAAGATCACGCCAGTGCACTCCATCCAGCATGGGAGACAGAGCAAGACTCCGTCTCA 280

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db        279 AAAAAAAAAA 270


RESULT 2
AG186502
LOCUS       AG186502                680 bp    DNA     linear   GSS 09-JAN-2002
DEFINITION  Pan troglodytes DNA, clone: RP43-060015.T7, genomic survey
            sequence.
ACCESSION   AG186502
VERSION     AG186502.1  GI:16716182
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library RPCI-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: T7
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-060015.T7"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
ORIGIN

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  Best Local Similarity   87.0%;  Pred. No. 1.4e-16;
  Matches  120;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||| ||||||||||  | |||||| |||||||| | ||||||||||||||||||||
Db        239 AGCTACTCGGGAGGCTGAGGAAAGAGAATTGCTTGAACTCAGGAGGCAGAGGTTGCAGTG 298

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||||| ||||||  ||||||| |||||||||||| |||||||||||||||||| |
Db        299 AGCCGAGATCATGCCACTGCACTCCATTCAGCCTGGGCGACAGAGCAAGACTCCGTCTGA 358

Qy        121 AAAAAAAAAATCGTTACA 138
              |||||||||| |  | ||
Db        359 AAAAAAAAAAAAGAAAAA 376


RESULT 3
AQ390169
LOCUS       AQ390169                418 bp    DNA     linear   GSS 06-MAR-1999
DEFINITION  CITBI-E1-2544A19.TF CITBI-E1 Homo sapiens genomic clone 2544A19,
            genomic survey sequence.
ACCESSION   AQ390169
VERSION     AQ390169.1  GI:4361192
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 418)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2544A19.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .418
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="2544A19"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

  Query Match             12.4%;  Score 107.6;  DB 8;  Length 418;
  Best Local Similarity   86.2%;  Pred. No. 3.6e-16;
  Matches  119;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||| |    ||||||||| || | ||||| |||||||||||||||||||||| |||||
Db         95 AGCTGCCTGAGAGGCTGAGGCATGGGAATCACTTGAACCCGGGAGGCAGAGGTTACAGTG 154

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||||||||||  |||||||||||||| ||| | ||||||||||||||||||||
Db        155 AGCCGAGATCACGCCACTGCACTCCATCCAGCCTAGGCAACAGAGCAAGACTCCGTCTCA 214

Qy        121 AAAAAAAAAATCGTTACA 138
              |||||||||| |   |||
Db        215 AAAAAAAAAAACAAAACA 232


RESULT 4
BM509394
LOCUS       BM509394                469 bp    mRNA    linear   EST 15-FEB-2002
DEFINITION  ih17f10.y1 Human insulinoma Homo sapiens cDNA 5' similar to
            SW:ALU8_HUMAN P39195 ALU SUBFAMILY SX SEQUENCE CONTAMINATION
            WARNING ENTRY. [1] ;, mRNA sequence.
ACCESSION   BM509394
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VERSION     BM509394.1  GI:18680537
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 469)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 416.
FEATURES             Location/Qualifiers
     source          1. .469
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Human insulinoma"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue  following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact  Hiroshi Inoue, MD/PhD for further
                     information on this library  (Metabolism Division, Permutt
                     Laboratory, Washington University School  of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110).  Note: this
                     is a Washington University Pancreas EST project library. "
ORIGIN
```

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  Query Match             12.4%;  Score 107.2;  DB 4;  Length 469;
  Best Local Similarity   81.6%;  Pred. No. 4.5e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||| |||| ||||||| | |   |||||||||||||||||| ||||||||||||||||||
Db        285 AGCCACTCGGGAGGCTTAAATGGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTG 344

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||  || |||||||||  |||||||||||||||||| || |||||||||||| |||||
Db        345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
              ||||||||||  | |   |   ||| ||  ||
Db        405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 5
BI468297
LOCUS       BI468297                516 bp    mRNA    linear   EST 11-MAR-2002
DEFINITION  id87b01.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:5022649
            5', mRNA sequence.
ACCESSION   BI468297
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VERSION     BI468297.1  GI:15284406
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 516)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            High quality sequence stop: 457.
FEATURES             Location/Qualifiers
     source          1. .516
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5022649"
                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Human insulinoma"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue  following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact  Hiroshi Inoue, MD/PhD for further
                     information on this library  (Metabolism Division, Permutt
                     Laboratory, Washington University School  of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110).  Note: this
                     is a Washington University Pancreas EST project library. "
ORIGIN
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  Query Match             12.4%;  Score 107.2;  DB 4;  Length 516;
  Best Local Similarity   81.6%;  Pred. No. 4.5e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Db        285 AGCCACTCGGGAGGCTTAAATGGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTG 344

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||  || |||||||||  |||||||||||||||||| || |||||||||||| |||||
Db        345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
              ||||||||||  | |   |   ||| ||  ||
Db        405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 6
BQ270800
LOCUS       BQ270800                529 bp    mRNA    linear   EST 15-JUL-2003
DEFINITION  ik05b06.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:5779930
            5', mRNA sequence.
ACCESSION   BQ270800
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VERSION     BQ270800.1  GI:20495866
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 529)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: ik05b06.x1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 428.
FEATURES             Location/Qualifiers
     source          1. .529
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5779930"
                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Human insulinoma"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Hiroshi Inoue, MD/PhD for further
                     information on this library (Metabolism Division, Permutt
                     Laboratory, Washington University School of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                     is a Washington University Pancreas EST project library. "
ORIGIN

  Query Match             12.4%;  Score 107.2;  DB 5;  Length 529;
  Best Local Similarity   81.6%;  Pred. No. 4.6e-16;
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Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Db        285 AGCCACTCGGGAGGCTTAAATGGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTG 344

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

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RESULT 7
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DEFINITION  ik02c03.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:5779589
            5', mRNA sequence.
ACCESSION   BQ267333
VERSION     BQ267333.1  GI:20492398
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 428.
FEATURES             Location/Qualifiers
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                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Hiroshi Inoue, MD/PhD for further
                     information on this library (Metabolism Division, Permutt
                     Laboratory, Washington University School of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                     is a Washington University Pancreas EST project library. "
ORIGIN

  Query Match             12.4%;  Score 107.2;  DB 5;  Length 556;
  Best Local Similarity   81.6%;  Pred. No. 4.6e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
              |||||||||| | |   |  ||| ||  ||
Db        405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 8
CK825308
LOCUS       CK825308                578 bp    mRNA    linear   EST 11-MAR-2004
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DEFINITION  ik02c03.y6 Human insulinoma Homo sapiens cDNA clone IMAGE:5779589
            5', mRNA sequence.
ACCESSION   CK825308
VERSION     CK825308.1  GI:44842233
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
            Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
            Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
            McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
            Bowers,Y.
  TITLE     WashU-Harvard Pancreas EST Project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            This read is a 5' RESEQUENCE of a previously sequenced pancreas
            clone
            This read has been verified (found to hit its original self in the
            correct orientation)
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Human insulinoma"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue  following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact  Hiroshi Inoue, MD/PhD for further
                     information on this library  (Metabolism Division, Permutt
                     Laboratory, Washington University School  of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110).  Note: this
                     is a Washington University Pancreas EST project library. "
ORIGIN

  Query Match             12.4%;  Score 107.2;  DB 7;  Length 578;
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  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Db        285 AGCCACTCGGGAGGCTTAAATGGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTG 344

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||  || |||||||||  |||||||||||||||||| || |||||||||||||| |||||
Db        345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
              ||||||||||  | |   |   ||| ||  ||
Db        405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 9
BU071662
LOCUS       BU071662                584 bp    mRNA    linear   EST 27-AUG-2002
DEFINITION  im32a11.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6036764
            5', mRNA sequence.
ACCESSION   BU071662
VERSION     BU071662.1  GI:22512851
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 584)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 428.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="IMAGE:6036764"
                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Human insulinoma"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue  following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact  Hiroshi Inoue, MD/PhD for further
                     information on this library  (Metabolism Division, Permutt
                     Laboratory, Washington University School  of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110).  Note: this
                     is a Washington University Pancreas EST project library. "
ORIGIN

  Query Match             12.4%;  Score 107.2;  DB 5;  Length 584;
  Best Local Similarity   81.6%;  Pred. No. 4.6e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Db        285 AGCCACTCGGGAGGCTTAAATGGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTG 344

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
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Db        405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 10
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LOCUS       BU782096                584 bp    mRNA    linear   EST 11-OCT-2002
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DEFINITION  im99h05.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6123129
            5', mRNA sequence.
ACCESSION   BU782096
VERSION     BU782096.1  GI:23825019
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 584)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 426.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="IMAGE:6123129"
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Human insulinoma"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Hiroshi Inoue, MD/PhD for further
                     information on this library (Metabolism Division, Permutt
                     Laboratory, Washington University School of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                     is a Washington University Pancreas EST project library. "
ORIGIN

  Query Match             12.4%;  Score 107.2;  DB 5;  Length 584;
  Best Local Similarity   81.6%;  Pred. No. 4.6e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
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Db        405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 11
BQ270346
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            5', mRNA sequence.
ACCESSION   BQ270346
VERSION     BQ270346.1  GI:20495412
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 427.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="Human insulinoma"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Hiroshi Inoue, MD/PhD for further
                     information on this library (Metabolism Division, Permutt
                     Laboratory, Washington University School of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                     is a Washington University Pancreas EST project library. "
ORIGIN

  Query Match             12.4%;  Score 107.2;  DB 5;  Length 589;
  Best Local Similarity   81.6%;  Pred. No. 4.6e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
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Db        405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 12
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BU783590
LOCUS       BU783590                589 bp    mRNA    linear   EST 11-OCT-2002
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            5', mRNA sequence.
ACCESSION   BU783590
VERSION     BU783590.1  GI:23827926
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: in06e04.x1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 428.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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                     /lab_host="DH10B (phage-resistant)"
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                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Hiroshi Inoue, MD/PhD for further
                     information on this library (Metabolism Division, Permutt
                     Laboratory, Washington University School of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                     is a Washington University Pancreas EST project library. "
ORIGIN

  Query Match            12.4%;  Score 107.2;  DB 5;  Length 589;
  Best Local Similarity  81.6%;  Pred. No. 4.6e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
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Db        405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436
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RESULT 13
BX507946
LOCUS       BX507946                564 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686L09262_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686L09262 5', mRNA sequence.
ACCESSION   BX507946
VERSION     BX507946.1  GI:32043918
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 564)
  AUTHORS   Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
  TITLE     EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I.,
            Wellenreuther,R., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686L09262) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
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ORIGIN

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Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Db        162 AGCTACTCGGGACGCTGAGGCAGGAGAATGGCGTGAACCCGGAAGGCGGAGCTTGCAGTG 221

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        222 AGCCGAGATCGCGCCACTGCACTCCATCCAGCCTGGGCGACAGAGCGAGACTCTGTCTCA 281

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGA 150
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Db        282 AAAGAAAAAAAAAAAAAAAAAGAAGAGTGGA 311


RESULT 14
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LOCUS       AQ428429                635 bp    DNA     linear   GSS 24-MAR-1999
DEFINITION  CITBI-E1-2564J3.TF CITBI-E1 Homo sapiens genomic clone 2564J3,
            genomic survey sequence.
ACCESSION   AQ428429
VERSION     AQ428429.1  GI:4496195
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 635)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2564J3.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
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                     /db_xref="taxon:9606"
                     /clone="2564J3"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

  Query Match             12.3%;  Score 106.4;  DB 8;  Length 635;
  Best Local Similarity   67.3%;  Pred. No. 7.3e-16;
  Matches  167;  Conservative    0;  Mismatches   76;  Indels    5;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||| ||||||| ||||| || ||||||| ||||||||||||||  |||||| |||||
Db        307 AGCTATTCAGGAGCCTGAGGCAGGAGAATCACTTGAACCCGGGAGGTGGAGGTTACAGTG 366

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        487 ACTAGCAGGAGTAAGATAAACTTAATTTATGATTTACCAAGTATTAATTTGATAATAATA 546

Qy        236 GGGAGATT 243
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Db        547 TAGACAGT 554


RESULT 15
CA428584/c
LOCUS       CA428584                679 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  UI-H-FE1-bez-l-08-0-UI.s1 NCI_CGAP_FE1 Homo sapiens cDNA clone
            UI-H-FE1-bez-l-08-0-UI 3', mRNA sequence.
ACCESSION   CA428584
VERSION     CA428584.1  GI:24791310
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 11-67, >MER47B#DNA/MER2_type (matched compliment)
            507-672, >ALU (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FE1-bez-l-08-0-UI"
                     /tissue_type="Cell lines"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FE1"
                     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
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                     Site_2: Not I; NCI_CGAP_FE1 is a normalized cDNA library
                     derived from a pool of mRNA obtained from 3 cell lines
                     from grade II chondrosarcoma tissues. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site.  Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CGCTACGGAC. The cell lines were provided by Dr James
                     Martin from the University of Iowa.
                     TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
                     TAG_LIB=UI-H-FE1
                     TAG_SEQ=CGCTACGGAC"
ORIGIN

  Query Match             12.2%;  Score 106;  DB 6;  Length 679;
  Best Local Similarity   84.9%;  Pred. No. 9.2e-16;
  Matches  118;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

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              ||| ||||  ||||||   |  ||||||| |||||||| ||||||||||||||||||||
Db        633 AGCCACTCGNGAGGCTTGAATGGGAGAATCACTTGAACCCTGGAGGCAGAGGTTGCAGTG 574

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||| || |||||||||  |||||||||||||||||| || ||||||||||||| |||||
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Qy        121 AAAAAAAAAATCGTTACAA 139
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Job time : 3696.27 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 15:59:17 ; Search time 595.011 Seconds
(without alignments)
8625.744 Million cell updates/sec

Title: US-09-601-267-36
Perfect score: 867
Sequence: 1 agctactcaggaggctgaga.....ccctaactgagaagggcgta 867

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	848.6	97.9	2426	2	AAV22994	Aav22994 DNA conta
4	848.6	97.9	2426	10	ADC21254	Adc21254 Plasmid p
5	834.6	96.3	2425	2	AAT11027	Aat11027 DNA encod
6	834.6	96.3	2425	2	AAT10283	Aat10283 Gene for
7	334	38.5	981	2	AAV41194	Aav41194 PstI frag
8	334	38.5	981	2	AAV19481	Aav19481 Human tel
9	333	38.4	980	4	AAS09471	Aas09471 Human DNA
10	333	38.4	981	6	AAD24234	Aad24234 Human tel
11	332.4	38.3	981	2	AAT89242	Aat89242 Clone con
12	332.4	38.3	981	2	AAV63644	Aav63644 Human tel
13	332.4	38.3	981	2	AAZ23626	Aaz23626 Human clo
14	332.4	38.3	981	3	AAA37564	Aaa37564 Human tel
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16	285	32.9	966	12	ADG82572	Adg82572 Human tel
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c 25	108.6	12.5	76698	12	ADJ84182	Adj84182 Human c-r
c 26	107	12.3	178024	12	ADQ97721	Adq97721 Human can
c 27	106.4	12.3	86764	12	ADQ97623	Adq97623 Human can
c 28	106.2	12.2	2275	10	ADB62299	Adb62299 Human cDN
c 29	106.2	12.2	313287	13	ABD33100	Abd33100 Human can
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39	104.8	12.1	26928	10	ADE82430	Ade82430 Human DNA
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41	104.8	12.1	26928	13	ADR47575	Adr47575 BAC clone
c 42	104.8	12.1	156843	11	ACN44786	Acn44786 Human gen
c 43	104.4	12.0	17570	8	ABZ74059	Abz74059 Secreted
c 44	104.4	12.0	17570	8	ADA98657	Ada98657 Human sec
c 45	104.4	12.0	17570	10	ABZ67655	Abz67655 Human sec

ALIGNMENTS

RESULT 1
AAZ07250
ID AAZ07250 standard; DNA; 867 BP.
XX
AC AAZ07250;
XX
DT 22-OCT-1999 (first entry)
XX
DE Human telomerase RNA gene (hTR) 5' flanking region.
XX
KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
KW gene therapy; thymidine kinase gene; anticancer therapy; human; ss.
XX
OS Homo sapiens.
XX
PN WO9938964-A2.
XX
PD 05-AUG-1999.
XX
PF 29-JAN-1999; 99WO-GB000308.
XX
PR 29-JAN-1998; 98GB-00001902.
XX
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI Keith WN;
XX
DR WPI; 1999-479183/40.
XX
PT Mouse and human telomerase RNA gene promoters, useful for tumor specific
PT gene therapy.
XX
PS Claim 3; Fig 4a; 109pp; English.
XX
CC The invention relates to promoter regions from mouse and human telomerase
CC RNA (TR) component genes. The TR gene promoter can be linked to a
CC heterologous gene, especially a gene encoding a cytotoxin, for therapy of
CC cancer, especially neoplasias. The telomerase is necessary for the
CC unrestricted proliferative capacity of many human cancers. Mutation or
CC dysregulation of the telomerase repression pathway may cause reactivation
CC or upregulation of telomerase expression in cancer. Substances,
CC identified in the methods, can be used to block transcription from the TR
CC gene promoter through interaction of the 5' regulatory sequences. These

```
CC   substances, e.g. antisense oligonucleotides, transcription factors,
CC   peptide nucleic acids and factors that disrupt signal transduction, are
CC   useful for cancer therapy. In particular, gene therapy vectors
CC   (especially pGT62-codAupp) comprising the promoter and a viral thymidine
CC   kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
CC   neoplasia can be controlled or treated. Direct down-regulation of
CC   telomerase RNA gene through manipulation of transcription factors may be
CC   effective anticancer therapy and the cloning of the hTR gene promoter
CC   allows the analysis of therapeutic molecules which modulate hTR promoter
CC   activity. The present sequence represents a human TR gene (hTR) 5'
CC   flanking sequence
XX
SQ   Sequence 867 BP; 237 A; 209 C; 221 G; 200 T; 0 U; 0 Other;

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Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
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Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
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Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
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Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
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RESULT 2
AAZ07247
ID   AAZ07247 standard; DNA; 1765 BP.
XX
AC   AAZ07247;
XX
DT   22-OCT-1999  (first entry)
XX
DE   Human telomerase RNA (hTR) gene sequence.
XX
KW   Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
KW   gene therapy; thymidine kinase gene; anticancer therapy; human; ss.
XX
OS   Homo sapiens.
XX
PN   WO9938964-A2.
XX
PD   05-AUG-1999.
XX
PF   29-JAN-1999;   99WO-GB000308.
XX
PR   29-JAN-1998;   98GB-00001902.
XX
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Keith WN;
XX
DR   WPI; 1999-479183/40.
XX
PT   Mouse and human telomerase RNA gene promoters, useful for tumor specific
PT   gene therapy.
XX
PS   Disclosure; Fig 1; 109pp; English.
XX
CC   The invention relates to promoter regions from mouse and human telomerase
CC   RNA (TR) component genes. The TR gene promoter can be linked to a
CC   heterologous gene, especially a gene encoding a cytotoxin, for therapy of
CC   cancer, especially neoplasias. The telomerase is necessary for the
CC   unrestricted proliferative capacity of many human cancers. Mutation or
CC   dysregulation of the telomerase repression pathway may cause reactivation
CC   or upregulation of telomerase expression in cancer. Substances,
CC   identified in the methods, can be used to block transcription from the TR
CC   gene promoter through interaction of the 5' regulatory sequences. These
CC   substances, e.g. antisense oligonucleotides, transcription factors,
CC   peptide nucleic acids and factors that disrupt signal transduction, are
CC   useful for cancer therapy. In particular, gene therapy vectors
CC   (especially pGT62-codAupp) comprising the promoter and a viral thymidine
CC   kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
CC   neoplasia can be controlled or treated. Direct down-regulation of
CC   telomerase RNA gene through manipulation of transcription factors may be
CC   effective anticancer therapy and the cloning of the hTR gene promoter
CC   allows the analysis of therapeutic molecules which modulate hTR promoter
CC   activity. The present sequence represents a human TR (hTR) gene sequence
XX
SQ   Sequence 1765 BP; 404 A; 458 C; 480 G; 423 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 867;  DB 2;  Length 1765;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-267;
  Matches  867;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420

Qy        421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||
Db        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
```

```
RESULT 3
AAV22994
ID   AAV22994 standard; DNA; 2426 BP.
XX
AC   AAV22994;
XX
DT   30-JUL-1998  (first entry)
XX
DE   DNA containing human telomerase RNA component gene sequences.
XX
KW   Human; telomerase RNA component gene sequence; ribonucleoprotein enzyme;
KW   cancer cell; telomerase activity; reporter construct;
KW   transcription regulatory region; prophylaxis; therapy;
KW   telomerase-related condition; chromatin position effect; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1234. .1245
FT                   /*tag=  f
FT                   /note= "beta-interferon response element"
FT   misc_feature    1238. .1259
FT                   /*tag=  b
FT                   /note= "PSE consensus sequence"
FT   misc_feature    1354. .1359
FT                   /*tag=  e
FT                   /note= "SP1 consensus sequence"
FT   CAAT_signal     1399. .1406
FT                   /*tag=  d
FT   misc_feature    1406. .1414
FT                   /*tag=  c
FT                   /note= "PSE consensus sequence"
FT   TATA_signal     1438. .1444
FT                   /*tag=  a
XX
PN   WO9811207-A2.
XX
PD   19-MAR-1998.
XX
PF   16-SEP-1997;   97WO-US016450.
XX
PR   16-SEP-1996;   96US-00714482.
XX
PA   (GERO-) GERON CORP.
XX
PI   Villeponteau B,  Harley C;
XX
DR   WPI; 1998-207376/18.
XX
PT   Human telomerase reporter constructs - useful in assays for regulators of
PT   mammalian telomerase expression.
XX
PS   Claim 6; Page 27-28; 59pp; English.
XX
CC   The present sequence contains human telomerase RNA component gene
CC   sequences. Telomerase is a ribonucleoprotein enzyme that synthesises one
CC   strand of the telomeric DNA using as a template a sequence contained
CC   within the RNA component of the enzyme. Most cancer cells express high
CC   levels of telomerase activity, while in normal somatic human cells,
CC   telomerase is not detected. The specification describes the production of
CC   a telomerase reporter construct which comprises a recombinant
CC   polynucleotide having a transcription regulatory region of a telomerase
CC   gene operably linked to a nucleotide sequence encoding a reporter
CC   polynucleotide heterologous to the transcription regulatory region.
CC   Expression of the reporter polynucleotide is detectable. The telomerase
CC   reporter construct is used in screening assays for determining modulators
CC   of transcription. The modulators can be used for prophylaxis or therapy
CC   of telomerase-related conditions. The reporter construct which has a
CC   selectable drug marker can be used to generate position effect reporter
CC   cells which can be used to determine whether a test agent inhibits
CC   chromatin position effect. Tagged RNA component constructs can be used to
CC   determine whether an agent modulates association between a mammalian RNA
CC   telomerase component and a mammalian telomerase
XX
SQ   Sequence 2426 BP; 620 A; 575 C; 650 G; 581 T; 0 U; 0 Other;

  Query Match             97.9%;  Score 848.6;  DB 2;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 2.1e-261;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840
```

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Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||
Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527
```

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RESULT 4
ADC21254
ID   ADC21254 standard; DNA; 2426 BP.
XX
AC   ADC21254;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Plasmid pGRN33 insert containing human TR DNA.
XX
KW   Viral vector; heterologous control element; gene expression;
KW   human telomerase reverse transcriptase; hTERT; tumour specific gene;
KW   cell death; transcriptional control element;
KW   human telomerase RNA component; hTR; cancer cell; liver cancer;
KW   prostate cancer; muscle cancer; neural cell cancer; lung cancer;
KW   pancreatic cancer; medulloblastoma; cervical carcinoma; fibrosarcoma;
KW   osteosarcoma; plasmid pGRN33; human; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003099616-A1.
XX
PD   29-MAY-2003.
XX
PF   25-JUL-2002; 2002US-00206447.
XX
PR   25-JUL-2001; 2001US-0308029P.
XX
PA   (IRVI/) IRVING J M.
PA   (KARP/) KARPF D B.
PA   (SCHI/) SCHIFF J M.
XX
PI   Irving JM,  Karpf DB,  Schiff JM;
XX
DR   WPI; 2003-730140/69.
XX
PT   New dual specificity vectors driven by the telomerase promoter, useful
PT   for killing or slowing the growth of tumor cells, or for treating cancer,
PT   e.g. liver cancer, prostate cancer, lung cancer, or pancreatic cancer.
XX
PS   Example 5; Page 20-21; 25pp; English.
XX
CC   The present invention relates to a viral vector comprising first and
CC   second genes controlled by heterologous control elements, where the first
CC   gene is preferentially expressed in cells expressing human telomerase
CC   reverse transcriptase (hTERT), and another gene under the control of a
CC   heterologous transcriptional control element for a tissue or tumour
CC   specific gene other than TERT, and where transduction of the vector into
CC   a mammalian cell expressing TERT causes the death of the cell or its
CC   progeny. In particular, the second gene may be under the control of a
CC   transcriptional control element for a tissue specific gene selected from
CC   albumin, alpha-fetoprotein, prostate-specific antigen, mitochondrial
CC   creatine kinase, myelin basic protein, glial fibrillary acidic protein,
CC   and neuron-specific enolase. The second gene may be under the control of
CC   a transcriptional control element for a human telomerase RNA component
CC   (hTR). The vector of the invention is useful for killing a cancer cell,
CC   or treating a subject for a condition associated with increased
CC   expression of TERT in affected cells. The vector is also useful in the
CC   preparation of a medicament for treatment of a condition associated with
CC   increased expression of TERT, particularly cancer, and especially liver
CC   cancer, prostate cancer, muscle cancer, neural cell cancer, lung cancer,
CC   pancreatic cancer, medulloblastoma, cervical carcinoma, fibrosarcoma, and
CC   osteosarcoma. The present sequence represents plasmid pGRN33 insert
CC   containing human TR DNA.
XX
SQ   Sequence 2426 BP; 620 A; 575 C; 650 G; 581 T; 0 U; 0 Other;
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  Query Match             97.9%;  Score 848.6;  DB 10;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 2.1e-261;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
                ||||||||||||||||||||||||||
Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527
```

RESULT 5
AAT11027
ID AAT11027 standard; DNA; 2425 BP.
XX
AC AAT11027;
XX
DT 09-JUN-1996 (first entry)
XX
DE DNA encoding the human telomerase RNA component.
XX
KW Telomerase; mammal; antisense; triplex forming oligonucleotide; plasmid;
KW probe; primer; ribozyme; ss.
XX
OS Homo sapiens.
XX
PN WO9601614-A2.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95WO-US008620.
XX
PR 07-JUL-1994; 94US-00272102.
PR 27-OCT-1994; 94US-00330123.
PR 13-FEB-1995; 95US-00387524.
PR 07-JUN-1995; 95US-00485778.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (GERO-) GERON CORP.
XX
PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C, Marhuenda MA;
PI Villeponteau B;
XX
DR WPI; 1996-097428/10.
XX
PT RNA components of (non)human mammalian telomerase(s) - useful in studying
PT cell senescence and immortalisation.
XX
PS Claim 37; Fig 1; 85pp; English.
XX
CC The RNA components of (non) human mammalian telomerase(s) especially from
CC mouse, rat and chinese hamster are all claimed. Antisense
CC oligonucleotides can be used to block the activity of the telomerase;
CC probes and primers can be used in detection; vectors and host cells
CC transformed with the isolated telomerase genes can be used for production
CC of telomerases; RNA and DNA ribozymes and triplex forming
CC oligonucleotides directed against the telomerase genes can be used
CC therapeutically as can plasmids. A mouse which lacks the telomerase gene
CC (also claimed) can be used for study of telomere regulation in vivo, and
CC the role it plays in immortalisation. This DNA sequence encodes the human
CC telomerase RNA component
XX
SQ Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 U; 0 Other;

  Query Match   96.3%; Score 834.6; DB 2; Length 2425;
  Best Local Similarity   99.0%; Pred. No. 6.7e-257;
  Matches 862; Conservative   0; Mismatches   4; Indels   5; Gaps   2;

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Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGC----GGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 836
```

```
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 1500

Qy        837 TTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||
Db       1501 TTTTTGTCTAACCCTAACTGAGAAGGGCGTA 1531


RESULT 6
AAT10283
ID   AAT10283 standard; DNA; 2425 BP.
XX
AC   AAT10283;
XX
DT   09-SEP-1996  (first entry)
XX
DE   Gene for RNA component of human telomerase.
XX
KW   RNA component; human; telomerase; lung fibroblast; cell line WI-38;
KW   recombinant production; synthesis; mutant; detection; mammalian;
KW   identification; modulating agent; neoplastic condition; gene;
KW   transcriptional regulatory sequence; gene therapy; disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9601835-A1.
XX
PD   25-JAN-1996.
XX
PF   06-JUL-1995;   95WO-US008530.
XX
PR   07-JUL-1994;   94US-00272102.
PR   27-OCT-1994;   94US-00330123.
PR   07-JUN-1995;   95US-00472802.
PR   07-JUN-1995;   95US-00482115.
XX
PA   (GERO-) GERON CORP.
XX
PI   Villeponteau B,  Feng J,  Funk W,  Andrews WH;
XX
DR   WPI; 1996-097581/10.
XX
PT   RNA component of mammalian telomerase, esp. human - useful in identifying
PT   e.g. candidate telomerase-modulating agents.
XX
PS   Claim 14; Page 97-98; 114pp; English.
XX
CC   The present sequence is the gene for the RNA component of human
CC   telomerase (RCHT), which was derived from a genomic DNA library obtd.
CC   from the human lung fibroblast cell line WI-38. The gene and the RCHT can
CC   be used in the recombinant prodn. of an active telomerase mol., capable
CC   of adding sequences to chromosomal DNA telomeres, and in the synthesis of
CC   mutant sequences for the detection of mutant mammalian telomerase RNA
CC   component polynucleotides. The RCHT may also be used in the
CC   identification of telomerase modulating agents, and in the detection of
CC   telomerase related, or neoplastic conditions in a patient.
CC   Polynucleotides of at least 25 consecutive nucleotides identical, or
CC   complementary to the RCHT sequence linked to heterologous transcriptional
CC   regulatory sequences, can be used for the gene therapy of human diseases
XX
SQ   Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 U; 0 Other;

  Query Match             96.3%;  Score 834.6;  DB 2;  Length 2425;
  Best Local Similarity   99.0%;  Pred. No. 6.7e-257;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    5;  Gaps    2;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| |||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGC----GGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 836
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 1500

Qy        837 TTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              ||||||||||||||||||||||||||||||||
Db       1501 TTTTTGTCTAACCCTAACTGAGAAGGGCGTA 1531


RESULT 7
AAV41194
ID   AAV41194 standard; DNA; 981 BP.
XX
AC   AAV41194;
XX
DT   08-OCT-1998  (first entry)
XX
DE   PstI fragment containing RNA component of human telomerase (hTR).
XX
KW   RNA component; human telomerase; antisense oligonucleotide; infection;
KW   neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW   contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW   immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    266. .716
```

```
FT                   /*tag=  a
FT                   /note= "RNA component of human telomerase (hTR)"
FT   misc_feature    311. .320
FT                   /*tag=  b
FT                   /note= "template region of hTR"
XX
PN   WO9828442-A1.
XX
PD   02-JUL-1998.
XX
PF   19-DEC-1997;   97WO-US023619.
XX
PR   20-DEC-1996;   96US-00770564.
PR   20-DEC-1996;   96US-00770565.
XX
PA   (GERO-) GERON CORP.
XX
PI   Kim NW,  Wu F,  Kealey JT,  Pruzan R,  Weinrich SL;
XX
DR   WPI; 1998-377670/32.
XX
PT   New polynucleotide(s) anti:sense to human telomerase - used for detecting
PT   or inhibiting human telomerase, e.g. for treating cancers, contraception,
PT   immuno-suppression or treating infection.
XX
PS   Disclosure; Page 53; 80pp; English.
XX
CC   This represents a PstI fragment containing the RNA component of human
CC   telomerase (hTR). The invention provides antisense oligonucleotides
CC   (AAV41169 to AAV41181) to hTR. These antisense oligonucleotides
CC   specifically hybridise to a nucleotide sequence within an accessible
CC   region of the hTR, but that does not hybridise to a sequence within the
CC   template region of hTR. These oligonucleotides may specifically be used
CC   for detection of an RNA component of human telomerase in a sample. This
CC   is useful for diagnosing cancer (especially neuroblastoma, bladder, colon
CC   and prostate cancer), and providing prognosis for a cancer patient. The
CC   inhibitory oligonucleotides can inhibit the telomerase activity level in
CC   a cell by interfering with transcription of the RNA component, decreasing
CC   the half-life of the telomerase RNA component transcript, inhibiting
CC   assembly of the RNA component into the telomerase holoenzyme, or
CC   inhibiting the polymerase activity of telomerase. These antisense
CC   oligonucleotides can be used for inhibiting telomerase activity in both
CC   cultured cells and in cells in vivo. They can be used in therapeutics for
CC   treating or preventing cancer, for contraception or sterilisation, for
CC   immunosuppression, and for selectively down-regulating specific branches
CC   of the immune system, e.g. a specific subset of T-cells, in anti-
CC   inflammatory therapies or for treating infections by, e.g. yeast,
CC   parasites or fungi
XX
SQ   Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 U; 0 Other;

  Query Match             38.5%;  Score 334;  DB 2;  Length 981;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-96;
  Matches  334;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||
Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 8
AAV19481
ID   AAV19481 standard; cDNA; 981 BP.
XX
AC   AAV19481;
XX
DT   28-AUG-1998  (first entry)
XX
DE   Human telomerase hTR gene.
XX
KW   Telomerase; hTR gene; TPC2; TPC3; telomere length; human; cancer;
KW   gene therapy; diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   unsure          21
FT                   /*tag=  a
FT   mRNA            266. .715
FT                   /*tag=  b
XX
PN   WO9811204-A1.
XX
PD   19-MAR-1998.
XX
PF   13-SEP-1996;   96WO-US014679.
XX
PR   13-SEP-1996;   96WO-US014679.
XX
PA   (GERO-) GERON CORP.
XX
PI   Villeponteau B,  Feng J,  Andrews WH,  Adams RR;
XX
DR   WPI; 1998-207373/18.
XX
PT   Human TPC2, TPC3 and TR genes - regulate telomere length or modulate
PT   telomerase activity.
XX
PS   Disclosure; Fig 9A-B; 86pp; English.
XX
CC   This nucleotide sequence comprises an approximately 1 kb PstI restriction
CC   fragment of plasmid pGRN33 that includes the human telomerase hTR gene.
CC   hTR3 mRNA levels correlate with telomerase activity levels in a variety
CC   or mortal and immortal cell lines. In methods of the invention,
CC   measurements of telomere length, telomerase activity or hTR levels can be
CC   used to identify immortal cells, such as cancer cells, and to evaluate
CC   the proliferative capacity of the cell. Gene therapy vectors encode
CC   useful nucleic acids such as hTR, or antisense nucleic acids or ribozymes
CC   that target TPC2, TPC3 (see AAV19479-80) and/or hTR gene products
XX
SQ   Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 U; 0 Other;

  Query Match             38.5%;  Score 334;  DB 2;  Length 981;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-96;
  Matches  334;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||
Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 9
AAS09471
ID   AAS09471 standard; DNA; 980 BP.
XX
AC   AAS09471;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human DNA containing the RNA component of telomerase.
XX
KW   Human; Telomerase; RNA component; vaccine; antibody; cancer; EF2H;
KW   nucleolin; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    21
FT                   /*tag=  a
FT                   /note= "Designated 0 in the specification, with 7 in the
FT                   complementary strand"
FT   misc_feature    311. .320
FT                   /*tag=  b
FT                   /label= Template_region
FT                   /note= "This region is not further defined in the
FT                   specification"
XX
PN   US6261556-B1.
XX
PD   17-JUL-2001.
XX
PF   18-OCT-1999;   99US-00420056.
XX
PR   04-AUG-1995;   95US-00510736.
PR   04-APR-1997;   97US-00833377.
XX
PA   (GERO-) GERON CORP.
XX
PI   Weinrich SL,  Atkinson EM,  Lichtsteiner SP,  Vasserot AP,  Pruzan RA;
PI   Kealey JT;
XX
DR   WPI; 2001-450477/48.
XX
PT   Purified human telomerase, useful for inducing immune response in
PT   animals, comprises several thousand folds increased purity compared with
PT   cytoplasmic crude cell preparations.
XX
PS   Disclosure; Col 9-12; 29pp; English.
XX
CC   The sequence contains human telomerase, hTR, RNA component. The invention
CC   relates to a purified human telomerase core enzyme protein comprising
CC   2000-fold increased purity compared with a crude extract of cells from
CC   adenovirus-transformed kidney cell line (293 cells) and when associated
CC   with telomerase RNA component has DNA polymerase activity and a molecular
CC   weight of 200-2000 kilo Daltons (kDa). The purified telomerase is useful
CC   for inducing a humoral or cell-mediated immune response in an animal.
CC   Purified telomerase or immunogenic fragments are useful as vaccines for
CC   treating diseases associated with over-expression of telomerase, such as
CC   cancer and for producing antibodies that recognize telomerase, which are
CC   useful as affinity agents in isolating the proteins and for detecting the
CC   presence of proteins in a sample, such as cell or tissue. Identification
CC   of telomerase aids in diagnosis of cancer or pre-cancerous states.
CC   Telomerase and/or telomerase associated proteins are also useful for
CC   screening compounds to identify agents that alter the association of
CC   telomerase-associated proteins, such as nucleolin or EF2H with telomerase
XX
SQ   Sequence 980 BP; 171 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

  Query Match             38.4%;  Score 333;  DB 4;  Length 980;
  Best Local Similarity   99.7%;  Pred. No. 7e-96;
  Matches  333;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCAGAGGATAGAAAAAAGNCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||
Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 10
AAD24234
ID   AAD24234 standard; DNA; 981 BP.
XX
AC   AAD24234;
XX
DT   07-MAR-2002  (first entry)
XX
DE   Human telomerase (hTR) gene.
XX
KW   Human; telomerase; TR; telomerase activity-related disease; therapy;
KW   cancer; pregnancy; fertility; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    267. .715
FT                   /*tag=  a
FT                   /note= "hTR transcript serves as template in the
FT                   telomerase ribonucleoprotein"
XX
PN   US6300110-B1.
XX
PD   09-OCT-2001.
XX
PF   23-DEC-1998;   98US-00220157.
XX
PR   09-SEP-1995;   95US-0003492P.
PR   05-JAN-1996;   96US-00583808.
PR   13-SEP-1996;   96US-00710249.
XX
PA   (GERO-) GERON CORP.
XX
PI   Villeponteau B,  Feng J,  Andrews WH,  Adams RR;
XX
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DR   WPI; 2002-033174/04.
XX
PT   Peptide products of the human TPC2 and TPC3 gene are involved in
PT   regulation of telomere length and activity are useful to diagnose and
PT   treat telomere length and activity-related diseases.
XX
PS   Example; Fig 9; 60pp; English.
XX
CC   The invention relates to methods and reagents for regulating telomere
CC   length and for modulating telomerase activity in mammalian cells. The
CC   invention also relates to purified, synthetic or recombinant peptides
CC   such as TPC2 or TPC3 used for detecting regulators of telomere length and
CC   telomerase activity in mammalian cells and for a variety of related
CC   diagnostic and therapeutic purposes. The method is useful for screening,
CC   diagnosing, monitoring and treating diseases and other conditions such as
CC   cancer, pregnancy, fertility, telomere length and telomerase-activity.
CC   The present sequence is human telomerase (hTR) gene
XX
SQ   Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

  Query Match             38.4%;  Score 333;  DB 6;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 7e-96;
  Matches  333;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCAGAGGATAGAAAAAAGNCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||
Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 11
AAT89242
ID   AAT89242 standard; DNA; 981 BP.
XX
AC   AAT89242;
XX
DT   12-MAY-1998  (first entry)
XX
DE   Clone containing hTR sequence.
XX
KW   Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW   inhibitor; human telomerase RNA; hTR; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 265. .716
FT                   /*tag= a
FT                   /note= "human telomerase RNA"
XX
PN   WO9738013-A1.
XX
PD   16-OCT-1997.
XX
PF   09-APR-1997;   97WO-US005931.
XX
PR   09-APR-1996;   96US-00630019.
XX
PA   (GERO-) GERON CORP.
XX
PI   Shay JW,  Wright WE,  Piatyszek MA,  Corey D,  Norton JC;
XX
DR   WPI; 1997-512647/47.
XX
PT   New peptide nucleic acids hybridising to mammalian telomerase RNA - used
PT   to inhibit telomerase, for treating tumours and other proliferative
PT   diseases, also for diagnosis.
XX
PS   Disclosure; Page 20-21; 76pp; English.
XX
CC   This fragment of cloned DNA contains the human telomerase RNA (hTR)
CC   sequence, (266-716bp). The hTR region contains a CCC template which the
CC   peptide nucleic acid (PNA) can recognise. The presence of a GGG in the
CC   PNAs allows for the specific hybridisation to the template region of this
CC   hTR component. PNAs can be used as probes to detect the RNA component of
CC   mammalian telomerase and as inhibitors of telomerase activity, especially
CC   in the treatment of cancer
XX
SQ   Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

  Query Match             38.3%;  Score 332.4;  DB 2;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-95;
  Matches  333;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
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Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
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Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
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Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||
Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 12
AAV63644
ID   AAV63644 standard; DNA; 981 BP.
XX
AC   AAV63644;
XX
DT   15-FEB-1999  (first entry)
XX
DE   Human telomerase RNA component sequence from lambda clone 28-1.
XX
KW   Lambda clone 28-1; human; telomerase RNA component; anticancer therapy;
KW   assay; vaccine; cancer; purification; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
```

```
FT   misc_feature    266. .716
FT                   /*tag=  a
FT                   /note= "human telomerase RNA component sequence"
XX
PN   WO9845450-A1.
XX
PD   15-OCT-1998.
XX
PF   04-APR-1997;   97WO-US006012.
XX
PR   04-APR-1997;   97WO-US006012.
XX
PA   (GERO-) GERON CORP.
XX
PI   Weinrich SL,  Atkinson EM,  Lichtsteiner SP,  Vasserot AP,  Pruzan RA;
PI   Kealey JT;
XX
DR   WPI; 1998-594485/50.
XX
PT   Purification of telomerase on affinity material - useful for, e.g.
PT   diagnosis and treatment of cancer.
XX
PS   Disclosure; Page 14-15; 76pp; English.
XX
CC   The present sequence represents the PstI fragment of the 2.4 kb SauIIIA1-
CC   HindIII fragment of lambda clone 28-1. This clone contains human
CC   telomerase RNA component gene sequences. The specification provides
CC   methods for purifying human telomerase. The methods involve the use of
CC   several sequential steps, including the use of two matrixes that bind
CC   molecules bearing negative charges, a matrix that binds molecules bearing
CC   positive charges, an affinity purification step and a size separation.
CC   Telomerase is a particular target of anticancer therapies, and is useful
CC   in assays for characterizing (pre)cancerous cells. The present sequence
CC   can be used for such assays. Telomerase can also be used to screen for
CC   specific modulators, for biochemical analysis of its activity, and in
CC   preparation of antibodies. Fragments of telomerase, or nucleic acid
CC   encoding them, are used in vaccines, and for treating over expression of
CC   telomerase, particularly in cancer
XX
SQ   Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

  Query Match             38.3%;  Score 332.4;  DB 2;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-95;
  Matches  333;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
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Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
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Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
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Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||
Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 13
AAZ23626
ID   AAZ23626 standard; DNA; 981 BP.
XX
AC   AAZ23626;
XX
DT   07-JAN-2000  (first entry)
XX
DE   Human clone 28-1 containing telomerase fragment.
XX
KW   Telomerase; human; immune response; cancer; vaccine; treatment; disease;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   US5968506-A.
XX
PD   19-OCT-1999.
XX
PF   04-APR-1997;   97US-00833377.
XX
PR   04-AUG-1995;   95US-00510736.
XX
PA   (GERO-) GERON CORP.
XX
PI   Atkinson EM,  Lichtsteiner SP,  Weinrich SL,  Pruzan RA,  Kealey JT;
PI   Vasserot AP;
XX
DR   WPI; 1999-590379/50.
XX
PT   Compositions comprising human telomerase, useful for treating diseases
PT   associated with overexpression of telomerase e.g. cancer.
XX
PS   Disclosure; Col 41-42; 34pp; English.
XX
CC   This invention describes a novel composition comprising human telomerase
CC   having at least 2000-fold (preferably at least 60000-fold) increased
CC   relative purity compared with crude extract of cells from adenovirus-
CC   transformed kidney cell line. The composition is useful for eliciting an
CC   immune response in animals and may therefore be used as a vaccine for
CC   treating diseases associated with the overexpression of telomerase e.g.
CC   cancer. This sequence represents a nucleic acid fragment from human clone
CC   28-1 which contains a fragment of the human telomerase described in the
CC   method of the invention
XX
SQ   Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

  Query Match             38.3%;  Score 332.4;  DB 2;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-95;
  Matches  333;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
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Db          1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
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Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
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Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
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Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
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Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334
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RESULT 14
AAA37564
ID   AAA37564 standard; DNA; 981 BP.
XX
AC   AAA37564;
XX
DT   15-AUG-2000  (first entry)
XX
DE   Human telomerase nucleotide sequence.
XX
KW   Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW   inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW   AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW   paternity testing; ds.
XX
OS   Homo sapiens.
XX
PN   US6046307-A.
XX
PD   04-APR-2000.
XX
PF   09-APR-1997;   97US-00838545.
XX
PR   09-APR-1996;   96US-00630019.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Wright WE,  Piatyszek MA,  Shay JW,  Norton JC,  Corey DR;
XX
DR   WPI; 2000-292432/25.
XX
PT   New peptide nucleic acid (PNA) compounds that inhibit telomerase activity
PT   in mammalian cells is useful as probes to detect the RNA component of a
PT   mammalian telomerase.
XX
PS   Disclosure; Col 13-14; 45pp; English.
XX
CC   The present sequence represents the human telomerase nucleotide sequence.
CC   The invention relates to peptide nucleic acid molecules which hybridise
CC   to the mRNA component of mammalian telomerase, and inhibit telomerase
CC   activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one
CC   strand of the telomeric DNA, using as a template an 11 nucleotide
CC   sequence contained within the RNA component of the enzyme. The invention
CC   relates to PNA molecules having a sequence of no more than 25 bases,
CC   which include the sequence GTTAGG. The uncharged nature of the PNA
CC   backbone increases the melting temperature of associating strands,
CC   increases the rate of association with targeted nucleic acids, and
CC   affords greater resistance of degradation by proteases or nucleases. The
CC   therapeutic PNAs may be used for treating disease conditions such as
CC   cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC   immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC   syndrome) and associated pathologies, fungal infections, and other
CC   diseases characterized by abnormal telomere metabolism or telomerase
CC   activity, in combination with antineoplastic and other cytotoxic or
CC   cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC   used for molecular diagnostics, labelled PNAs are used as hybridization
CC   probes to detect or quantitate polynucleotides having a human telomerase
CC   RNA (hTR) sequence. PNA probes are also used for forensic identification
CC   of individuals, e.g. paternity testing, based on hTR gene restriction
CC   fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC   probes to detect the RNA component of a mammalian telomerase and as
CC   inhibitors of telomerase activity. The method of the present invention
CC   allows cancerous conditions to be detected with increased confidence and
CC   possibly at an earlier stage, before cells are detected as cancerous
CC   based on pathological characteristics. The diagnostic and prognostic
CC   methods of the present invention can be used to detect an immortal or
CC   neoplastic cell or tumour tissue or cancer of any origin, provided the
CC   cell expresses telomerase activity and its RNA component
XX
SQ   Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

  Query Match           38.3%;  Score 332.4;  DB 3;  Length 981;
  Best Local Similarity 99.7%;  Pred. No. 1.1e-95;

  Matches  333;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
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Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
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Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
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Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
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Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 15
AAS15442
ID   AAS15442 standard; DNA; 981 BP.
XX
AC   AAS15442;
XX
DT   14-FEB-2002  (first entry)
XX
DE   PstI fragment containing human telomerase RNA component gene sequence.
XX
KW   Mammalian; forensic; paternity testing; human telomerase RNA component;
KW   hTR gene RFLP pattern; cancer; inflammation; lymphoproliferative disease;
KW   autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia;
KW   HIV; AIDS; human immunodeficiency virus; telomere metabolism; cytostatic;
KW   acquired immunodeficiency syndrome; anti-inflammatory; immunosuppressive;
KW   bacteriophage lambda clone 28-1; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    266. .716
FT                   /*tag=  a
FT                   /note= "htr gene sequence"
FT   misc_feature    311. .320
FT                   /*tag=  b
FT                   /note= "Template region of hTR used as template for
FT                   synthesis of telomeric repeats"
XX
PN   US6294650-B1.
XX
PD   25-SEP-2001.
XX
PF   08-JUL-1999;   99US-00349532.
XX
PR   09-APR-1996;   96US-00630019.
PR   09-APR-1997;   97US-00838545.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Shay JW,  Wright WE,  Piatyszek MA,  Corey DR,  Norton JC;
XX
DR   WPI; 2001-638024/73.
XX
PT   New peptide nucleic acids that hybridizes to the RNA component of
PT   mammalian telomerase, useful for treating or preventing cancer,
PT   inflammation, lymphoproliferative diseases, autoimmune disease, or
```

PT neurodegenerative diseases.
XX
PS Disclosure; Col 13-16; 46pp; English.
XX
CC The present invention relates to peptide nucleic acids (PNAs), comprising
CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in
CC mammalian cells by hybridising to the RNA component of mammalian
CC telomerase. The PNAs are useful as probes to detect the RNA component of
CC mammalian telomerase and as inhibitors of telomerase activity, or to
CC detect and/or quantitate polynucleotide having the human telomerase RNA
CC component (hTR) sequence, as well as in forensic identification of
CC individuals, such as paternity testing or identification of criminal
CC suspects or unknown descendants based on the hTR gene RFLP pattern. The
CC PNA can be further used for treating or preventing cancer, inflammation,
CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC diseases. The PNAs in combination with other pharmaceuticals (such as
CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC diseases characterised by abnormal telomere metabolism or telomerase
CC activity. The present sequence represents a PstI fragment, derived from
CC bacteriophage lambda clone 28-1, containing the hTR gene sequence
XX
SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 0 U; 1 Other;

Query Match 38.3%; Score 332.4; DB 4; Length 981;
Best Local Similarity 99.7%; Pred. No. 1.1e-95;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
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Db          1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
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Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
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Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
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Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
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Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||
Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334
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Job time : 600.011 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:01:02 ; Search time 4148.84 Seconds
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Title: US-09-601-267-36
Perfect score: 867
Sequence: 1 agctactcaggaggctgaga.....ccctaactgagaagggcgta 867

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	867	100.0	867	6	AX019582	AX019582 Sequence
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c	6	860.6	99.3	47601	9	AC078802	AC078802 Homo sapi
	7	848.6	97.9	2420	6	I31750	I31750 Sequence 3
	8	848.6	97.9	2426	6	AR016035	AR016035 Sequence
	9	848.6	97.9	2426	6	AR059196	AR059196 Sequence
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	37	115.6	13.3	188571	9	AC107956	AC107956 Homo sapi
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	39	114	13.1	115812	9	AC004796	AC004796 Homo sapi
c	40	113.6	13.1	176550	9	AL356356	AL356356 Human DNA
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	42	111.4	12.8	188741	9	AC002542	AC002542 Homo sapi
	43	110.8	12.8	68275	9	AC073335	AC073335 Homo sapi
c	44	110.8	12.8	128501	9	AC012614	AC012614 Homo sapi
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ALIGNMENTS

RESULT 1
BD225833
LOCUS BD225833 867 bp DNA linear PAT 17-JUL-2003
DEFINITION Promoter region of mouse and human telomerase RNA component genes.
ACCESSION BD225833
VERSION BD225833.1 GI:33035603
KEYWORDS JP 2002509699-A/36.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 867)
AUTHORS Keith,W.N.
TITLE Promoter region of mouse and human telomerase RNA component genes
JOURNAL Patent: JP 2002509699-A 36 02-APR-2002;
CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD
COMMENT OS Homo sapiens (human)
PN JP 2002509699-A/36
PD 02-APR-2002
PF 29-JAN-1999 JP 2000529424
PR 29-JAN-1998 GB 9801902.9
PI WILLIAM NICOL KEITH
PC
C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K38/00,A61K45/00, PC A61K48/00,
PC A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02 PC ,C12Q1/68//C12N9/12,
PC (A61K35/76,A61K31:522),C12N15/00,A61K37/02,C12N5/00 CC
Promoter region of mouse and human telomerase RNA component CC genes
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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ORIGIN

Query Match 100.0%; Score 867; DB 6; Length 867;
Best Local Similarity 100.0%; Pred. No. 3.7e-238;

Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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RESULT 2
AX019582
LOCUS AX019582 867 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 36 from Patent WO9938964.
ACCESSION AX019582
VERSION AX019582.1 GI:10043496
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Keith,W.N.
TITLE Promoter regions of the mouse and human telomerase rna component genes
JOURNAL Patent: WO 9938964-A 36 05-AUG-1999;
KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES Location/Qualifiers
source 1. .867
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 867; DB 6; Length 867;
Best Local Similarity 100.0%; Pred. No. 3.7e-238;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
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Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
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Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
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Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867


RESULT 3
BD225798
LOCUS       BD225798               1765 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Promoter region of mouse and human telomerase RNA component genes.
ACCESSION   BD225798
VERSION     BD225798.1  GI:33035568
KEYWORDS    JP 2002509699-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1765)
  AUTHORS   Keith,W.N.
  TITLE     Promoter region of mouse and human telomerase RNA component genes
  JOURNAL   Patent: JP 2002509699-A 1 02-APR-2002;
            CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002509699-A/1
            PD   02-APR-2002
            PF   29-JAN-1999 JP 2000529424
            PR   29-JAN-1998 GB    9801902.9
            PI   WILLIAM NICOL KEITH
            PC
            C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K38/00,A61K45/00, PC
             A61K48/00,
            PC   A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02 PC
            ,C12Q1/68//C12N9/12,
            PC   (A61K35/76,A61K31:522),C12N15/00,A61K37/02,C12N5/00 CC
            Promoter region of mouse and human telomerase RNA component  CC
              genes
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.3e-238;
  Matches  867;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
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RESULT 4
AX019547
LOCUS       AX019547               1765 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9938964.
ACCESSION   AX019547
VERSION     AX019547.1  GI:10043461
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Keith,W.N.
  TITLE     Promoter regions of the mouse and human telomerase rna component
            genes
  JOURNAL   Patent: WO 9938964-A 1 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES             Location/Qualifiers
     source          1. .1765
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ORIGIN

  Query Match           100.0%;  Score 867;  DB 6;  Length 1765;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-238;
  Matches  867;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
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Db        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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RESULT 5
AF047386
LOCUS       AF047386                1765 bp    DNA     linear   PRI 02-APR-1998
DEFINITION  Homo sapiens telomerase RNA (TR) gene, promoter and complete
            sequence.
ACCESSION   AF047386
VERSION     AF047386.1  GI:3005555
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1765)
  AUTHORS   Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
            Black,D.M. and Keith,W.N.
  TITLE     Cloning and characterization of human and mouse telomerase RNA gene
            promoter sequences
  JOURNAL   Oncogene 16 (10), 1345-1350 (1998)
  MEDLINE   98206512
  PUBMED    9546436
REFERENCE   2  (bases 1 to 1765)
  AUTHORS   Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
            Black,D.M. and Keith,W.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-1998) Medical Oncology, Beatson Institute,
            Switchback Rd, Glasgow G61 1BD, UK
FEATURES             Location/Qualifiers
     source          1. .1765
                     /organism="Homo sapiens"
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     gene            1. .1248
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ORIGIN
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  Best Local Similarity  100.0%;  Pred. No. 4.3e-238;
  Matches  867;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
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Db        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
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Db        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
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Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
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Db        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
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Db        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
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Db        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
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Db        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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RESULT 6
AC078802/c
LOCUS AC078802 47601 bp DNA linear PRI 01-MAR-2003
DEFINITION Homo sapiens 3 BAC RP11-816J6 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
ACCESSION AC078802
VERSION AC078802.14 GI:28626602
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 47601)
AUTHORS Muzny,D.M., Adams,C.; Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D., Nelson,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 47601)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 47601)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 4 (bases 1 to 47601)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Mar 1, 2003 this sequence version replaced gi:28467099.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

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/db_xref="taxon:9606"
/chromosome="3"
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/note="overlaps bases 1. .2097 of clone AC007849"
/function="clone overlap"
repeat_region complement(4. .792)
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repeat_region complement(808. .1090)
/rpt_family="AluJb"
repeat_region complement(1091. .1550)
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/rpt_family="L1"
repeat_region 1845. .2993

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                     /rpt_family="AluSc"
     repeat_region   3112. .3262
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     repeat_region   complement(3316. .4136)
                     /rpt_family="L1P"
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Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db      36334 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 36275

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
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Db      36274 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 36215

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
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Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
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Db      36094 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 36035

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
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Qy        421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
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Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
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Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
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Db      35794 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 35735

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
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Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
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Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
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Db      35614 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 35555

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db      35554 TGTCTAACCCTAACTGAGAAGGGCGTA 35528


RESULT 7
I31750
LOCUS       I31750                 2420 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 3 from patent US 5583016.
ACCESSION   I31750
VERSION     I31750.1  GI:1822541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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           Unclassified.
REFERENCE  1  (bases 1 to 2420)
  AUTHORS  Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE    Mammalian telomerase
  JOURNAL  Patent: US 5583016-A 3 10-DEC-1996;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             97.9%;  Score 848.6;  DB 6;  Length 2420;
  Best Local Similarity   99.4%;  Pred. No. 8.9e-233;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
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Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
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Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
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Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
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Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
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Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 8
AR016035
LOCUS       AR016035               2426 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 3 from patent US 5776679.
ACCESSION   AR016035
VERSION     AR016035.1  GI:3972312
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2426)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Assays for the DNA component of human telomerase
  JOURNAL   Patent: US 5776679-A 3 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .2426
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             97.9%;  Score 848.6;  DB 6;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 8.9e-233;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
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Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
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Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
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Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
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Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
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Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||
Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 9
AR059196
LOCUS       AR059196                2426 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5837857.
ACCESSION   AR059196
VERSION     AR059196.1  GI:5984773
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2426)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 5837857-A 3 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .2426
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           97.9%;  Score 848.6;  DB 6;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 8.9e-233;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
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Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
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Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
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Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
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Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
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Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
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Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
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Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 10
AR075507
LOCUS       AR075507                2426 bp    DNA     linear   PAT 30-AUG-2000
DEFINITION  Sequence 4 from patent US 5958680.
ACCESSION   AR075507
VERSION     AR075507.1  GI:10002257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2426)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 5958680-A 4 28-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .2426
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           97.9%;  Score 848.6;  DB 6;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 8.9e-233;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
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Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
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Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
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Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 11
AR081664
LOCUS       AR081664                2426 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 1 from patent US 5972605.
ACCESSION   AR081664
VERSION     AR081664.1  GI:10008390
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2426)
  AUTHORS   Villeponteau,B. and Harley,C.
  TITLE     Assays for regulators of mammalian telomerase expression
  JOURNAL   Patent: US 5972605-A 1 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .2426
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             97.9%;  Score 848.6;  DB 6;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 8.9e-233;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
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Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
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Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
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Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
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Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
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Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 12
AR161905
LOCUS       AR161905                2426 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 3 from patent US 6258535.
ACCESSION   AR161905
VERSION     AR161905.1  GI:16228915
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2426)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 6258535-A 3 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .2426
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             97.9%;  Score 848.6;  DB 6;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 8.9e-233;
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Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
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Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
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Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
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Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
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Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 13
AR306455
LOCUS       AR306455               2426 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from patent US 6548298.
ACCESSION   AR306455
VERSION     AR306455.1  GI:31696294
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.

REFERENCE   1  (bases 1 to 2426)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 6548298-A 3 15-APR-2003;
FEATURES             Location/Qualifiers
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  Query Match           97.9%;  Score 848.6;  DB 6;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 8.9e-233;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
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Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
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Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527
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RESULT 14
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LOCUS       BD176144                2425 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Mammalian telomerase.
ACCESSION   BD176144
VERSION     BD176144.1  GI:29121848
KEYWORDS    JP 2002272489-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2425)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: JP 2002272489-A 3 24-SEP-2002;
            GERON CORP
COMMENT     OS   Unidentified
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            PD   24-SEP-2002
            PF   06-MAR-2002 JP 2002061125
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            07-JUN-1995 US    08/472802,07-JUN-1995 US    08/482115 PI   BRYANT
            VILLEPONTEAU,JUNLI FENG,WALTER FUNK,WILLIAM H ANDREWS PC
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            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Qy        837 TTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
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RESULT 15
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LOCUS       AR081665                981 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 2 from patent US 5972605.
ACCESSION   AR081665
VERSION     AR081665.1  GI:10008391
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 981)
  AUTHORS   Villeponteau,B. and Harley,C.
  TITLE     Assays for regulators of mammalian telomerase expression
  JOURNAL   Patent: US 5972605-A 2 26-OCT-1999;
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ORIGIN

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Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
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Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
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	5	105	12.1	53779	2	PCT-US04-42189-85	Sequence 85, Appl
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c	10	103.4	11.9	27069	11	US-11-073-360-1602	Sequence 1602, Ap
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	15	102.8	11.9	1790242	13	US-60-660-322-2216	Sequence 2216, Ap
	16	102.4	11.8	80436	13	US-60-659-397-12235	Sequence 12235, A
	17	102	11.8	18564	9	US-10-472-963-1608	Sequence 1608, Ap
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c	19	101.4	11.7	180283	1	PCT-US05-10257-703	Sequence 703, App
	20	101.2	11.7	61009	13	US-60-659-397-11881	Sequence 11881, A
	21	101.2	11.7	125038	13	US-60-659-397-11980	Sequence 11980, A
	22	101.2	11.7	166133	13	US-60-659-397-11887	Sequence 11887, A
	23	100.8	11.6	9428	11	US-11-033-545-634	Sequence 634, App
c	24	100.6	11.6	380780	13	US-60-660-322-2217	Sequence 2217, Ap
c	25	100.4	11.6	99624	13	US-60-659-397-12123	Sequence 12123, A
c	26	100	11.5	38703	11	US-11-052-544-28	Sequence 28, Appl
c	27	99.8	11.5	28668	2	PCT-US04-42189-121	Sequence 121, App
	28	99.6	11.5	1768	9	US-10-472-963-184	Sequence 184, App
	29	99.6	11.5	5940	13	US-60-651-235-1681	Sequence 1681, Ap
	30	99.6	11.5	6944	13	US-60-651-235-1683	Sequence 1683, Ap
	31	99.6	11.5	6944	13	US-60-651-235-1684	Sequence 1684, Ap
	32	99.6	11.5	7043	13	US-60-651-235-1685	Sequence 1685, Ap
	33	99.6	11.5	7044	13	US-60-651-235-1682	Sequence 1682, Ap
	34	99.6	11.5	145616	1	PCT-US05-10257-222	Sequence 222, App
c	35	99.4	11.5	116750	13	US-60-660-711-33	Sequence 33, Appl
	36	99.2	11.4	150147	1	PCT-US05-10257-799	Sequence 799, App
c	37	99.2	11.4	221420	13	US-60-659-397-12132	Sequence 12132, A
	38	99	11.4	26060	1	PCT-US05-10257-795	Sequence 795, App
c	39	98.6	11.4	48889	13	US-60-659-397-11973	Sequence 11973, A
	40	98.4	11.3	73170	13	US-60-660-557-58	Sequence 58, Appl
c	41	98.2	11.3	201	13	US-60-660-322-5830	Sequence 5830, Ap
c	42	98.2	11.3	240309	13	US-60-660-322-2210	Sequence 2210, Ap
c	43	98.2	11.3	252209	13	US-60-660-884-35	Sequence 35, Appl
	44	98	11.3	601	11	US-11-033-545-3591	Sequence 3591, Ap
	45	98	11.3	601	11	US-11-033-545-10358	Sequence 10358, A

ALIGNMENTS

RESULT 1
US-10-948-947A-1/c
; Sequence 1, Application US/10948947A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Freier, Susan M.
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Gaarde, William A.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Swayze, Eric E.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: ANTISENSE INHIBITION VIA RNASE H-INDEPENDENT REDUCTION IN mRNA
; FILE REFERENCE: ISPH-0871
; CURRENT APPLICATION NUMBER: US/10/948,947A
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: 60/392,020
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 10/461,163
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 76698
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: antisense oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 15311-15410
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 15414
; OTHER INFORMATION: n = A,T,C or G
US-10-948-947A-1

Query Match 12.5%; Score 108.6; DB 9; Length 76698;
Best Local Similarity 81.3%; Pred. No. 5.3e-15;
Matches 126; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60

```
Db      15588 AGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGGCGGAGCTTGCAGTG 15529

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||||| |||||| |||||| |||||||||||||| ||||| |||||| ||||||
Db      15528 AGCCGAGATCATGCCACTGCACTCCAACCAGCCTGGGCGACAGAGCGAGACTCTGTCTCA 15469

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACT 155
              ||||||||||     | ||    | |  || | | |
Db      15468 AAAAAAAAAAAAAAAAAAAAAAGAGGCAGGCTAAGT 15434


RESULT 2
US-60-659-397-12140/c
; Sequence 12140, Application US/60659397
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/659,397
;  CURRENT FILING DATE:  2005-03-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12140
;   LENGTH: 47154
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(47154)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-60-659-397-12140

  Query Match             12.2%;  Score 106;  DB 13;  Length 47154;
  Best Local Similarity   88.5%;  Pred. No. 1.9e-14;
  Matches  115;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||| || |||||| || |||||| ||||||| ||| ||||||||
Db       1099 AGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAGGCGGAGCTTGCAGTG 1040

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||||| |||||| |||||| |||||||||||||| ||||| |||||| ||||||
Db       1039 AGCCGAGATCATGCCACTGCACTCCAACCAGCCTGGGCGACAGAGCGAGACTCTGTCTCA 980

Qy        121 AAAAAAAAAA 130
              |||||||| |
Db        979 AAAAAAAAGA 970


RESULT 3
US-60-660-714-33
; Sequence 33, Application US/60660714
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Ming-Yi Chiang
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Ravi Jain
;  TITLE OF INVENTION: COMPOSITIONS AND THEIR USES DIRECTED TO PROTEIN BINDING ACTIVITY
;  FILE REFERENCE: DPTK-0076US.L
;  CURRENT APPLICATION NUMBER: US/60/660,714
;  CURRENT FILING DATE:  2005-03-10
;  NUMBER OF SEQ ID NOS: 1025
;  SOFTWARE: PatentSeq version 1.0
; SEQ ID NO 33
;   LENGTH: 48701
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 7486-7585
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 36591-36690
;   OTHER INFORMATION: n is a, c, g, or t
US-60-660-714-33

  Query Match             12.2%;  Score 106;  DB 13;  Length 48701;
  Best Local Similarity   88.5%;  Pred. No. 1.9e-14;
  Matches  115;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||  |||||||||| || |||||||||||||||||| |||||| ||||||||||||
Db      25254 AGCTACTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCGGAGGTTGCAGTG 25313

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||  |||||||  |||||  |||||||||||||||| | ||||  |||||||  |||||
Db      25314 AGCCAAGATCACACCACTGTACTCCATCCAGCCTGGGCAACAGAGTGAGACTCCATCTCA 25373

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db      25374 AAAAAAAAAA 25383


RESULT 4
PCT-US04-42189-127/c
; Sequence 127, Application PC/TUS0442189
; GENERAL INFORMATION:
;  APPLICANT: Bayer Healthcare LLC
;  APPLICANT:  Beard, Chris
;  APPLICANT:  Burgess, Chris
;  APPLICANT:  Gannon, Allison
;  APPLICANT:  Harvey, Jeanne
;  APPLICANT:  Lechner, John F.
;  APPLICANT:  Li, Zheng
;  TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
;  FILE REFERENCE: 1657/2038
;  CURRENT APPLICATION NUMBER: PCT/US04/42189
;  CURRENT FILING DATE:  2004-12-15
;  PRIOR APPLICATION NUMBER: US 10/765,790
;  PRIOR FILING DATE: 2004-01-27
;  PRIOR APPLICATION NUMBER: US 10/737,082
;  PRIOR FILING DATE: 2003-12-16
;  NUMBER OF SEQ ID NOS: 300
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
;   LENGTH: 294575
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US04-42189-127

  Query Match             12.2%;  Score 106;  DB 2;  Length 294575;
  Best Local Similarity   88.5%;  Pred. No. 2.3e-14;
  Matches  115;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||| || |||||||||||||||| |||| || ||||||||||||
Db     124842 AGCTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAAGCGGAGGTTGCAGTG 124783

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||  |||||||||||| | ||| |||||||||||||| ||||||| ||| ||| |||||
Db     124782 AGTGGAGATCACGCCATTGCACTTCATCCAGCCTGGGCAAAAGAGCGAGATTCCATCTCA 124723

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db     124722 AAAAAAAAAA 124713


RESULT 5
```

```
PCT-US04-42189-85
; Sequence 85, Application PC/TUS0442189
; GENERAL INFORMATION:
;  APPLICANT: Bayer Healthcare LLC
;  APPLICANT:  Beard, Chris
;  APPLICANT:  Burgess, Chris
;  APPLICANT:  Gannon, Allison
;  APPLICANT:  Harvey, Jeanne
;  APPLICANT:  Lechner, John F.
;  APPLICANT:  Li, Zheng
;  TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
;  FILE REFERENCE: 1657/2038
;  CURRENT APPLICATION NUMBER: PCT/US04/42189
;  CURRENT FILING DATE:  2004-12-15
;  PRIOR APPLICATION NUMBER: US 10/765,790
;  PRIOR FILING DATE: 2004-01-27
;  PRIOR APPLICATION NUMBER: US 10/737,082
;  PRIOR FILING DATE: 2003-12-16
;  NUMBER OF SEQ ID NOS: 300
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
;   LENGTH: 53779
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US04-42189-85

  Query Match             12.1%;  Score 105;  DB 2;  Length 53779;
  Best Local Similarity   88.4%;  Pred. No. 3.3e-14;
  Matches  114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 GCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGA 61
              |||||||||||||||| | || |||||| |||||||||| |||||  ||| |||||  |||
Db      10336 GCTACTCAGGAGGCTGTGGCAGGAGAATGGCTTGAACCCAGGAGGTGGAGCTTGCAATGA 10395

Qy         62 GCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCAA 121
              |||||||||| ||||||  |||||||||||||| |||| ||||| |||||||||||||
Db      10396 GCCGAGATCATGCCACTGCACTCCATCCAGCCTGAGCGACAGAGCGAGACTCCGTCTCAA 10455

Qy        122 AAAAAAAAA 130
              |||||||||
Db      10456 AAAAAAAAA 10464


RESULT 6
US-09-543-771-6
; Sequence 6, Application US/09543771
; GENERAL INFORMATION:
;  APPLICANT: John P. Carulli et al.
;  TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3
;  FILE REFERENCE: 032796-013
;  CURRENT APPLICATION NUMBER: US/09/543,771
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 09/229,319
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 60/071,449
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: US 60/105,511
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 62
; SEQ ID NO 6
;   LENGTH: 26928
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (12044),(12489),(26433),(26434),(26435),(26436),(26439),(26441)
;   OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-543-771-6

  Query Match             12.1%;  Score 104.8;  DB 6;  Length 26928;
  Best Local Similarity   81.8%;  Pred. No. 3.4e-14;
  Matches  121;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||  |||||||||| || |||||| || |||||| |||||| ||| ||||||||
Db       3207 AGCTACTTGGGAGGCTGAGGCAGGAGAATGGCGTGAACCTGGGAGGCGGAGCTTGCAGTG 3266

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||  |||||||  |||||||||||||||||||||| ||||  ||||||||||||
Db       3267 AGCCGAGATTGCGCCACTGCACTCCATCCAGCCTGGGCGACAGAGTTAGACTCCGTCTCA 3326

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTG 148
              ||||||||||     | ||  |  | ||
Db       3327 AAAAAAAAAAAAAAAAAAAAAATTAGCTG 3354


RESULT 7
US-10-472-963-1206/c
; Sequence 1206, Application US/10472963
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Human Secreted Proteins
;  FILE REFERENCE: PS954PCT
;  CURRENT APPLICATION NUMBER: US/10/472,963
;  CURRENT FILING DATE:  2003-09-25
;  PRIOR APPLICATION NUMBER: PCT/US02/09370
;  PRIOR FILING DATE: 2002-03-26
;  PRIOR APPLICATION NUMBER: US 60/278,650
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: US 09/950,082
;  PRIOR FILING DATE: 2001-09-12
;  PRIOR APPLICATION NUMBER: US 09/950,083
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 1834
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1206
;   LENGTH: 17570
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-472-963-1206

  Query Match             12.0%;  Score 104.4;  DB 9;  Length 17570;
  Best Local Similarity   87.7%;  Pred. No. 4e-14;
  Matches  114;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||| ||||||| || || |||||| || ||||||| ||| |||||| ||||||||
Db       4158 AGCTACTCGGGAGGCTTAGGCAGGAGAATGGCATGAACCCAGGACGCAGAGCTTGCAGTG 4099

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||  |||||  |||||||  |||||||||||||||| || |||||  ||||||||||||
Db       4098 AGCCAAGATCGCGCCACTGCACTCCATCCAGCCTGGGAGACAGAGCGAGACTCCGTCTCA 4039

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db       4038 AAAAAAAAAA 4029


RESULT 8
US-10-960-414-122
; Sequence 122, Application US/10960414
; GENERAL INFORMATION:
;  APPLICANT: MILLER, LANCE D.
;  APPLICANT:  GEORGE, JOSHY
;  APPLICANT:  VEGA, VINSENSIUS B.
;  TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
;  TITLE OF INVENTION:  PROGNOSIS, AND DIAGNOSIS OF CANCERS
;  FILE REFERENCE: 38271-76067
;  CURRENT APPLICATION NUMBER: US/10/960,414
;  CURRENT FILING DATE:  2004-10-06
;  NUMBER OF SEQ ID NOS: 500
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 122
;   LENGTH: 141540
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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```
US-10-960-414-122

  Query Match             12.0%;  Score 104.4;  DB 7;  Length 141540;
  Best Local Similarity   87.7%;  Pred. No. 4.9e-14;
  Matches  114;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||| |||||||| || ||||||| |||||||  || |||| ||||||||||||
Db     109682 AGCTACTCAGAAGGCTGAGGCAGGAGAATCACTTGAACGGGGAAGGCGGAGGTTGCAGTG 109741

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              | || |||||| ||||||  |||||||||||||||| || ||||||||||||| |||||
Db     109742 AACCAAGATCAAGCCACTGAACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 109801

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db     109802 AAAAAAAAAA 109811


RESULT 9
US-10-479-874A-9/c
; Sequence 9, Application US/10479874A
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: CHDs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
;  FILE REFERENCE: EX02-090C-US
;  CURRENT APPLICATION NUMBER: US/10/479,874A
;  CURRENT FILING DATE:  2003-12-04
;  PRIOR APPLICATION NUMBER: US 60/296,076
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/328,605
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/338,733
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/357,253
;  PRIOR FILING DATE: 2002-02-15
;  PRIOR APPLICATION NUMBER: US 60/357,600
;  PRIOR FILING DATE: 2002-02-15
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 142519
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-479-874A-9

  Query Match             12.0%;  Score 103.8;  DB 9;  Length 142519;
  Best Local Similarity   79.4%;  Pred. No. 6.7e-14;
  Matches  123;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||| ||||||||||  | |||||| || |||||||||||||| ||| ||||||||
Db      33770 AGCTACTCGGGAGGCTGAGGTAGGAGAATGGCGTGAACCCGGGAGGCGGAGCTTGCAGTG 33711

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              || ||||||| |||||||  |||||||||||||||| |||| ||||| |||||| ||||||
Db      33710 AGTCGAGATCGCGCCACTGCACTCCATCCAGCCTGAGCGACAGAGCGAGACTCTGTCTCA 33651

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACT 155
              |||| ||||||    |  |  ||   |  || | |
Db      33650 AAAATAAAAATAAAAAATAAATAAAATAAATAAAT 33616


RESULT 10
US-11-073-360-1602/c
; Sequence 1602, Application US/11073360
; GENERAL INFORMATION:
;  APPLICANT: SHIFFMAN, Dov et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001586
;  CURRENT APPLICATION NUMBER: US/11/073,360
;  CURRENT FILING DATE:  2005-03-07
;  NUMBER OF SEQ ID NOS: 17377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1602
;   LENGTH: 27069
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-073-360-1602

  Query Match             11.9%;  Score 103.4;  DB 11;  Length 27069;
  Best Local Similarity   77.6%;  Pred. No. 6.9e-14;
  Matches  125;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||| || ||||||||||||||||||||||||||||||||||||||
Db       1532 AGCTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 1473

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||| |||||| | |||||  |||||||||||||||| || ||||  |||||   ||  |
Db       1472 AGCTGAGATCGCACCACTGTACTCCATCCAGCCTGGGTGACAGAGTGAGACTGTCTCAAA 1413

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTC 161
              |||||| | |        ||  | ||  ||  | ||   |||
Db       1412 AAAAAAGAGAAACAGCTAAGGTCTGTGGGTCTCCTGGGCTC 1372


RESULT 11
US-60-660-817-127/c
; Sequence 127, Application US/60660817
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Ming-Yi Chiang
;  APPLICANT:  Lex M. Cowsert
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  APPLICANT:  Christine Esau
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Ravi Jain
;  APPLICANT:  Erich Koller
;  APPLICANT:  Brett P. Monia
;  APPLICANT:  Susan J. Myers
;  APPLICANT:  Hong Zhang
;  TITLE OF INVENTION: Compositions and Their Uses Directed To Nucleic Acid Regulators
;  FILE REFERENCE: DPTK-0078US.L
;  CURRENT APPLICATION NUMBER: US/60/660,817
;  CURRENT FILING DATE:  2005-03-10
;  NUMBER OF SEQ ID NOS: 2650
;  SOFTWARE: PatentSeq version 1.0
; SEQ ID NO 127
;   LENGTH: 105001
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-660-817-127

  Query Match             11.9%;  Score 103.4;  DB 13;  Length 105001;
  Best Local Similarity   87.6%;  Pred. No. 8e-14;
  Matches  113;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||| |||||||||| || |||||| || ||||||| |||||| ||| ||||||||
Db      58428 AGCTACTCGGGAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGGCGGAGCTTGCAGTG 58369

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||  |||||||  ||||||||||||||||||||| ||||| ||||||||||||
Db      58368 AGCCGAGATTGCGCCACTGCACTCCATCCAGCCTGGGCGACAGAGCGAGACTCCGTCTCA 58309

Qy        121 AAAAAAAAA 129
              |||||  ||
Db      58308 AAAAATGAA 58300


RESULT 12
US-60-660-322-10597
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```
; Sequence 10597, Application US/60660322
; GENERAL INFORMATION:
;  APPLICANT: LUKE, May et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001572
;  CURRENT APPLICATION NUMBER: US/60/660,322
;  CURRENT FILING DATE:  2005-03-11
;  NUMBER OF SEQ ID NOS: 28070
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10597
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-660-322-10597

  Query Match             11.9%;  Score 102.8;  DB 13;  Length 201;
  Best Local Similarity   82.9%;  Pred. No. 5.7e-14;
  Matches  116;  Conservative    1;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||| |||||||||| | |||||| || |||||||||||||||||| ||| ||||
Db         25 AGCTACTTGGGAGGCTGAGGCGGGAGAATGGCGTGAACCCGGGAGGCAGAGCTTGTAGTG 84

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              | | |||||||||||||:| |||||||||||||||| |||| ||||| |||||| ||||||
Db         85 ACCGGAGATCACGCCAMTGAACTCCATCCAGCCTGAGCGACAGAGCGAGACTCGGTCTCA 144

Qy        121 AAAAAAAAAATCGTTACAAT 140
              ||||||||||     | |||
Db        145 AAAAAAAAAAAAAAAAAAAT 164


RESULT 13
US-60-659-397-11949/c
; Sequence 11949, Application US/60659397
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  CHANG, Sheng-Yung
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
;  TITLE OF INVENTION:  VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001470
;  CURRENT APPLICATION NUMBER: US/60/659,397
;  CURRENT FILING DATE:  2005-03-09
;  NUMBER OF SEQ ID NOS: 47859
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11949
;   LENGTH: 19732
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-659-397-11949

  Query Match             11.9%;  Score 102.8;  DB 13;  Length 19732;
  Best Local Similarity   86.9%;  Pred. No. 9.1e-14;
  Matches  113;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||| ||||||| || || |||||||||||||||||||||||| ||||||| ||||
Db      15909 AGCTACTCGGGAGGCTAAGGCAGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGTAGTG 15850

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||   |||||| |||||||||| ||| || || ||||| |||||| ||||||
Db      15849 AGCCGAGATTGTGCCACTGCACTCCATCCAACCTAGGTGACAGAGCGAGACTCTGTCTCA 15790

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db      15789 AAAAAAAAAA 15780


RESULT 14
US-11-028-539-63
; Sequence 63, Application US/11028539
; GENERAL INFORMATION:
;  APPLICANT: ALLIEL, Patrick
;  APPLICANT:  PERIN, Jean-Pierre
;  APPLICANT:  RIEGER, Francois
;  TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AND DEDUCED PROTEIN SEQUENCE FAMILY WITH HU
;  TITLE OF INVENTION:  ENDOGENOUS RETROVIRAL MOTIFS
;  FILE REFERENCE: 200936US0PCT
;  CURRENT APPLICATION NUMBER: US/11/028,539
;  CURRENT FILING DATE:  2005-01-05
;  PRIOR APPLICATION NUMBER: US/09/719,554
;  PRIOR FILING DATE: 2001-01-18
;  PRIOR APPLICATION NUMBER: PCT/FR99/01513
;  PRIOR FILING DATE: 1999-06-25
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 44100
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-028-539-63

  Query Match             11.9%;  Score 102.8;  DB 11;  Length 44100;
  Best Local Similarity   86.9%;  Pred. No. 9.9e-14;
  Matches  113;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||| |||||||||||||| |||||| |||||||||| |||||  ||||||||||||
Db      40085 AGCTACTTGGGAGGCTGAGACAGGAGAATTGCTTGAACCCAGGAGGTGGAGGTTGCAGTG 40144

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||  | |||||  |||||||||||||||||| | |||||  |||||  ||||||
Db      40145 AGCCGAGATTGCACCACTGCACTCCATCCAGCCTGGGCCACAGAGCGAGACTGTGTCTCA 40204

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db      40205 AAAAAAAAAA 40214


RESULT 15
US-60-660-322-2216
; Sequence 2216, Application US/60660322
; GENERAL INFORMATION:
;  APPLICANT: LUKE, May et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE, METHODS OF DETECTION AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001572
;  CURRENT APPLICATION NUMBER: US/60/660,322
;  CURRENT FILING DATE:  2005-03-11
;  NUMBER OF SEQ ID NOS: 28070
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2216
;   LENGTH: 1790242
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1790242)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-60-660-322-2216

  Query Match             11.9%;  Score 102.8;  DB 13;  Length 1790242;
  Best Local Similarity   82.9%;  Pred. No. 1.5e-13;
  Matches  116;  Conservative    1;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||| |||||||||| | |||||| || |||||||||||||||||| ||| ||||
Db    1209396 AGCTACTTGGGAGGCTGAGGCGGGAGAATGGCGTGAACCCGGGAGGCAGAGCTTGTAGTG 1209455

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              | | |||||||||||||:| |||||||||||||||| |||| ||||| |||||| ||||||
```

```
Db    1209456 ACCGGAGATCACGCCAMTGAACTCCATCCAGCCTGAGCGACAGAGCGAGACTCGGTCTCA 1209515

Qy        121 AAAAAAAAAATCGTTACAAT 140
              ||||||||||     | |||
Db    1209516 AAAAAAAAAAAAAAAAAAAT 1209535
```

Search completed: April 26, 2005, 22:37:32
Job time : 467.827 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:01:33 ; Search time 2673.73 Seconds
(without alignments)
8940.469 Million cell updates/sec

Title: US-09-601-267-37
Perfect score: 628
Sequence: 1 tgtgaccttgaactacagac.....ttctcgctgacttccagcgg 628

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	79	12.6	2876	3	AK085092	AK085092 Mus muscu
	2	76	12.1	624	2	BB660202	BB660202 BB660202
c	3	61.8	9.8	286	6	CB937393	CB937393 IpCGJx13_
	4	61.2	9.7	290	9	CR139916	CR139916 Reverse s
	5	58.8	9.4	729	9	AG451206	AG451206 Mus muscu
c	6	58.2	9.3	323	5	BU535156	BU535156 AGENCOURT
	7	58.2	9.3	743	9	AG612453	AG612453 Mus muscu
	8	58.2	9.3	1281	9	AG349913	AG349913 Mus muscu
	9	57.8	9.2	735	9	AG458145	AG458145 Mus muscu
	10	57.8	9.2	1301	9	AG346181	AG346181 Mus muscu
	11	57.6	9.2	759	9	AG539897	AG539897 Mus muscu
	12	57.6	9.2	766	9	AG429109	AG429109 Mus muscu
	13	57.4	9.1	735	9	AG602238	AG602238 Mus muscu
	14	57.4	9.1	802	9	AG604663	AG604663 Mus muscu
	15	57	9.1	743	9	AG591362	AG591362 Mus muscu
	16	57	9.1	774	9	AG284698	AG284698 Mus muscu
	17	56.8	9.0	359	2	BF552926	BF552926 UI-R-C2-n
c	18	56.8	9.0	409	1	AI072290	AI072290 UI-R-C2-n
	19	56.6	9.0	1101	9	CNS01537	AL104941 Drosophil
c	20	56.4	9.0	535	9	CE837523	CE837523 tigr-gss-
	21	56.2	8.9	737	9	AG530686	AG530686 Mus muscu
	22	56.2	8.9	772	9	AG539394	AG539394 Mus muscu
	23	56.2	8.9	811	9	AG567668	AG567668 Mus muscu
	24	56.2	8.9	1213	9	AG341273	AG341273 Mus muscu
	25	55.8	8.9	732	9	AG492128	AG492128 Mus muscu
	26	55.6	8.9	761	9	AG574939	AG574939 Mus muscu
c	27	55.4	8.8	391	9	CE835556	CE835556 tigr-gss-
	28	55.4	8.8	716	9	AG398550	AG398550 Mus muscu
	29	55.4	8.8	1172	9	AG324265	AG324265 Mus muscu
	30	55.2	8.8	786	9	AG564579	AG564579 Mus muscu
	31	55.2	8.8	1319	9	CL644695	CL644695 CH213-79A
	32	55	8.8	662	9	AG481539	AG481539 Mus muscu
	33	55	8.8	1456	9	AG435703	AG435703 Mus muscu
c	34	54.8	8.7	585	4	BG928544	BG928544 HNC68-1-E
	35	54.8	8.7	720	9	AG280906	AG280906 Mus muscu
	36	54.8	8.7	782	9	AG474197	AG474197 Mus muscu
	37	54.8	8.7	802	9	AG459758	AG459758 Mus muscu
	38	54.8	8.7	1215	9	AG448698	AG448698 Mus muscu
	39	54.6	8.7	713	9	AG345270	AG345270 Mus muscu
c	40	54.6	8.7	824	8	BZ258789	BZ258789 CH230-479
	41	54.6	8.7	839	9	AG518301	AG518301 Mus muscu
	42	54.6	8.7	1120	9	AG332349	AG332349 Mus muscu
	43	54.4	8.7	741	9	AG473256	AG473256 Mus muscu
	44	54.4	8.7	802	9	AG484854	AG484854 Mus muscu
	45	54.4	8.7	1150	9	AG288203	AG288203 Mus muscu

ALIGNMENTS

RESULT 1
AK085092
LOCUS AK085092 2876 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430035J07 product:telomerase RNA component, full insert sequence.
ACCESSION AK085092
VERSION AK085092.1 GI:26102453
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research

```
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2876)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .2876
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:D430035J07"
                     /db_xref="taxon:10090"
                     /clone="D430035J07"
                     /tissue_type="lung"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="13 days embryo"
     misc_feature    1. .2876
                     /note="telomerase RNA component (MGD|MGI:109558,
                     GB|AF047387, evidence: BLASTN, 98%, match=2480)"
ORIGIN

  Query Match             12.6%;  Score 79;  DB 3;  Length 2876;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-07;
  Matches   79;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        550 ACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTT 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTT 61

Qy        610 TCTCGCTGACTTCCAGCGG 628
              ||||||||||||||||||||
Db         62 TCTCGCTGACTTCCAGCGG 80


RESULT 2
BB660202
LOCUS       BB660202                624 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB660202 RIKEN full-length enriched, 13 days embryo lung Mus
            musculus cDNA clone D430035J07 5', mRNA sequence.
ACCESSION   BB660202
VERSION     BB660202.1  GI:16494023
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 624)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
            Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
            and Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
            Sugahara,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
            Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .624
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="D430035J07"
                     /tissue_type="lung"
                     /dev_stage="13 days embryo"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, 13 days embryo
                     lung"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with BamHI and XhoI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."
ORIGIN

  Query Match             12.1%;  Score 76;  DB 2;  Length 624;
```

```
  Best Local Similarity   100.0%;  Pred. No. 2.4e-06;
  Matches   76;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        553 TAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTTTCT 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTTTCT 60

Qy        613 CGCTGACTTCCAGCGG 628
              ||||||||||||||||
Db         61 CGCTGACTTCCAGCGG 76


RESULT 3
CB937393/c
LOCUS       CB937393                286 bp    mRNA    linear   EST 29-APR-2003
DEFINITION  IpCGJx13_16_A08_23 IpCGJx13 Ictalurus punctatus cDNA clone
            IpCGJx13_16_A08 5', mRNA sequence.
ACCESSION   CB937393
VERSION     CB937393.1  GI:30222784
KEYWORDS    EST.
SOURCE      Ictalurus punctatus (channel catfish)
  ORGANISM  Ictalurus punctatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
            Ictaluridae; Ictalurus.
REFERENCE   1  (bases 1 to 286)
  AUTHORS   Bengten,E., Khayat,M., Middleton,D., Waldbieser,G., Askovic,S.,
            Jensen,K.T., Warr,G., Miller,N., Clem,L.W. and Wilson,M.
  TITLE     Identification of expressed genes in mixed leukocyte culture and in
            a macrophage cell line in channel catfish, Ictalurus punctatus
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Waldbieser GC
            Catfish Genetics Research Unit
            USDA-Agricultural Research Service
            141 Experiment Station Road, Stoneville, MS 38776, USA
            Tel: 662 686 3593
            Fax: 662 686 3567
            Email: gwaldbieser@ars.usda.gov
            Single pass sequencing. Bases called with Phred v0.000925.c. Low
            quality bases and vector trimmed with Lucy v1.16.
            Plate: 16  row: A  column: 8
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .286
                     /organism="Ictalurus punctatus"
                     /mol_type="mRNA"
                     /strain="commercial"
                     /db_xref="taxon:7998"
                     /clone="IpCGJx13_16_A08"
                     /cell_type="peripheral blood leucocyte"
                     /cell_line="MLC52-1"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="IpCGJx13"
                     /note="Organ: peripheral blood; Vector: pSport1; Site_1:
                     Sal 1; Site_2: Not 1; Primary library"
ORIGIN

  Query Match             9.8%;  Score 61.8;  DB 6;  Length 286;
  Best Local Similarity   62.7%;  Pred. No. 0.0033;
  Matches   96;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy        231 TTTTTTTTTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTT 290
              |||||||||||||||||||||||||   |  || |    | ||||  ||      | |   |
Db        230 TTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGATTCAGCGATTTTAATAGAACATCAATA 171

Qy        291 CAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTG 350
              |||   |   | ||   ||   || |   |    |||| ||| ||| ||||||||||
Db        170 ACACTGAGGCTAAGTTTTAAATAAAACCGGAATGTGTGTGTGTGTGTGTGTGTGTGTG 111

Qy        351 TGTATGTGTGTGTGTCTCACAGCAAGAAACAGA 383
              ||| ||||||||||   | ||  ||| | |||
Db        110 TGTGTGTGTGTGTGTGAGAGAGAGAGAGAGAGA 78


RESULT 4
CR139916
LOCUS       CR139916                290 bp    DNA     linear   GSS 06-JUL-2004
DEFINITION  Reverse strand read from insert in 3'HPRT insertion targeting and
            chromosome engineering clone MHPP77c16, genomic survey sequence.
ACCESSION   CR139916
VERSION     CR139916.1  GI:49887788
KEYWORDS    GSS; genome survey sequence; MICER.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 290)
  AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES             Location/Qualifiers
     source          1. .290
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="MHPP77c16"
                     /clone_lib="MHPP"
ORIGIN

  Query Match             9.7%;  Score 61.2;  DB 9;  Length 290;
  Best Local Similarity   76.5%;  Pred. No. 0.0045;
  Matches   75;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy        327 TGTGCGTGCGTGCGTGTGTGTGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTT 386
              |||| ||| ||| ||||||||||||| |||| |||||||||| ||||  ||| ||||
Db        168 TGTGTGTGTGTGTGTGTGTGTGTGTGTGAGTGTGTCTCAGAGCACTAAAGAGATAA 227

Qy        387 TATTATTTATTTTTTATTTATTTATTTTTTGCAAGTGA 424
              | ||||| |||||| ||||| ||  | |  | || ||
Db        228 AAATATTTTTTTTTTTTTTATATAGATATATCGAGAGA 265


RESULT 5
AG451206
LOCUS       AG451206                729 bp    DNA     linear   GSS 04-JUN-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-336B17.T7, genomic survey
            sequence.
ACCESSION   AG451206
VERSION     AG451206.1  GI:48152720
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     BAC end Sequences of Library MSMg01
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 729)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
```

```
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .729
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-336B17.T7"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             9.4%;  Score 58.8;  DB 9;  Length 729;
  Best Local Similarity   58.6%;  Pred. No. 0.015;
  Matches   75;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy        289 TTCAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTG 348
              | | | | | | |||||| ||||| |||||       |||| ||| ||| |||||||||
Db        432 TACCAGTTTGGAATATTTAAGAAAATAAGCCGTGTGTGTGTGTGTGTGTGTGTGTGTG 491

Qy        349 TGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATT 408
              ||||| |||||||                 || |  ||  || ||| ||| ||
Db        492 TGTGTGTGTGTGTNNNNNNNNNNNNNNNNNNNNNTNNNNTTTTNTTTNTTTNTTTTTTTTT 551

Qy        409 TATTTTTT 416
              | ||||||
Db        552 TTTTTTTT 559


RESULT 6
BU535156/c
LOCUS       BU535156                323 bp    mRNA    linear   EST 13-SEP-2002
DEFINITION  AGENCOURT_10185537 NIH_MGC_126 Homo sapiens cDNA clone
            IMAGE:6562631 5', mRNA sequence.
ACCESSION   BU535156
VERSION     BU535156.1  GI:22845597
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 323)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: NCI
             cDNA Library Preparation: Michael Brownstein Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2738  row: p  column: 23
            High quality sequence stop: 322.
FEATURES             Location/Qualifiers
     source          1. .323
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6562631"
                     /tissue_type="mixed (pool of 40 RNAs)"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC_126"
                     /note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
                     Site_2: SfiI (ggccgcctcggcc); Double-stranded cDNA was
                     prepared from a pool of 40 cell line polyA+ RNAs (bladder
                     - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
                     4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
                     kidnney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
                     5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
                     salivary gland - 1.3%, and skin - 2.3%).  5' and 3'
                     adaptors were used in cloning as follows:
                     5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'.  Full-length
                     enriched library was constructed using the Clontech
                     Creator SMART kit and size-selected to contain the 0.5-1
                     kb size fraction (other fractions present in NIH_MGC_127
                     and NIH_MGC_128).  Library created in the laboratory of T.
                     Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             9.3%;  Score 58.2;  DB 5;  Length 323;
  Best Local Similarity   64.0%;  Pred. No. 0.021;
  Matches   87;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy        232 TTTTTTTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTC 291
              |||||||||||||||||||||||  |  |  |     |||    ||||  |   || |
Db        315 TTTTTTTTTTTTTTTTTTTTTTTTTNTACGATTTTAAGATGTTTAATACTCAATTTTGC 256

Qy        292 AACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGT 351
              |  || |  |||| | |  | |  |  ||     | | ||||| ||| ||||||||||||
Db        255 ACTTCAAAAATATATTAAGAGCTGATTCTGTTGAAAGAGCGTGTGTGTGTGTGTGTGTGT 196

Qy        352 GTATGTGTGTGTGTCT 367
              || | |||||||||| |
Db        195 GTGTCTGTGTGTGTGT 180


RESULT 7
AG612453
LOCUS       AG612453                743 bp    DNA     linear   GSS 05-JUN-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-547P24.T7, genomic survey
            sequence.
ACCESSION   AG612453
VERSION     AG612453.1  GI:48373283
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     BAC end Sequences of Library MSMg01
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 743)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
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     source          1. .743
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-547P24.T7"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             9.3%;  Score 58.2;  DB 9;  Length 743;
  Best Local Similarity   52.7%;  Pred. No. 0.021;
  Matches  126;  Conservative    0;  Mismatches  113;  Indels    0;  Gaps    0;

Qy        129 ATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCGCCACTTTTCCCCAC 188
              || |  ||  | |||| |||  |||| |||| ||||||  | ||  |||||  | |||  |
Db         51 ATTCCACTTGCGTCTGACTCCTAAATGCTGGGATTAAAACTGTGTGCCACCATACCCAGC 110

Qy        189 TTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTTTTTTTTTTT 248
               | ||     | |   |   |  |   | |     |  ||| ||| || || ||
Db        111 AGCAACAATGATTTTTATTAAATGTTTAAACTAATAAGTTTACATTTATTTATTATTATT 170

Qy        249 TTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAGTATATTTCA 308
               |||   | |      ||||  | ||   | |   |   |  | |     | | ||
Db        171 ATTTAATGGGTGGGGTGGGGTAAATGCTCAAAGTGCCTGTGCTATGTTTCCACTGGTACA 230

Qy        309 GAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTATGTGTGTGTCT 367
               | |  |    |      |||| ||| ||| ||||||||||||| |||||||||| |
Db        231 CATAATACATGTGCCCATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 289


RESULT 8
AG349913
LOCUS       AG349913               1281 bp    DNA     linear   GSS 02-JUN-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-146F15.TJ, genomic survey
            sequence.
ACCESSION   AG349913
VERSION     AG349913.1  GI:47923223
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     BAC end Sequences of Library MSMg01
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1281)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : TJ
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .1281
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-146F15.TJ"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             9.3%;  Score 58.2;  DB 9;  Length 1281;
  Best Local Similarity   63.7%;  Pred. No. 0.021;
  Matches   72;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy        304 TTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTATGTGTGTGT 363
              |||| |||   || | ||   | | || ||| ||| |||||||||||||| |||||||||
Db        245 TTTCTGAAGTAAAACTTCTAGGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 304

Qy        364 GTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTT 416
              || |                |  | || ||| ||||||  || ||| ||||||
Db        305 GTGTNNNNNNNNNNNNTTNNTNNTTTTTTTTTTTTTTTTNNTTTTTTTTTTTT 357


RESULT 9
AG458145
LOCUS       AG458145               735 bp    DNA     linear   GSS 04-JUN-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-345E14.T7, genomic survey
            sequence.
ACCESSION   AG458145
VERSION     AG458145.1  GI:48149659
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     BAC end Sequences of Library MSMg01
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 735)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-345E14.T7"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             9.2%;  Score 57.8;  DB 9;  Length 735;
  Best Local Similarity   55.5%;  Pred. No. 0.026;
  Matches  101;  Conservative    0;  Mismatches   81;  Indels    0;  Gaps    0;
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Qy        235 TTTTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAAC 294
              ||||| |||||| |  || |     |  |  |     ||  |   |  |   | ||
Db        188 TTTTTCTTTTTTATAATTCTTTGTTAGGACAGCTTTTTTTGGTCTTTGTTTATGTATTT 247

Qy        295 TCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTA 354
              | |  |   |||  ||  |  ||  |      |||| ||| ||| ||||||||||||||
Db        248 TATTTTCAGTTTTGGATTCTCAGTGTATATTCTGTGTGTGTGTGTGTGTGTGTGTG 307

Qy        355 TGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTT 414
              |||||||||||  |                  |||| || ||| |||||| ||| ||| ||||
Db        308 TGTGTGTGTGTGTNTNTNNNNNTTTTTTTTTTTTTNTTTNTTTTTTTTTTTTTTTTTT 367

Qy        415 TT 416
              ||
Db        368 TT 369
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RESULT 10
AG346181
LOCUS AG346181 1301 bp DNA linear GSS 02-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-141E03.TJ, genomic survey sequence.
ACCESSION AG346181
VERSION AG346181.1 GI:47919491
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1301)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
source 1. .1301
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-141E03.TJ"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

Query Match 9.2%; Score 57.8; DB 9; Length 1301;
Best Local Similarity 67.6%; Pred. No. 0.026;
Matches 71; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

```
Qy        312 ACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTATGTGTGTGTCTCACA 371
              || || || |||   |||| ||| ||| ||||||||||||| |||||||||| |
Db        226 ACAAATCCACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTNN 285

Qy        372 GCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTT 416
              |||| || ||| || ||| ||| ||| ||||||
Db        286 NNNTNNNNTNNTTTTTTTTTTTTTTNTTTTTTTTTTTTTTTTT 330
```

RESULT 11
AG539897
LOCUS AG539897 759 bp DNA linear GSS 05-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-452L08.TJ, genomic survey sequence.
ACCESSION AG539897
VERSION AG539897.1 GI:48300311
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 759)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
source 1. .759
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
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/db_xref="taxon:57486"
/clone="MSMg01-452L08.TJ"
/sex="male"
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ORIGIN

Query Match 9.2%; Score 57.6; DB 9; Length 759;
Best Local Similarity 62.7%; Pred. No. 0.028;
Matches 84; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Qy        283 CCTACTTTCAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTG 342
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Db        458 CCAACAAAGAACTATTGACTAAACGGGAGTCCCAGTGTAAAACGTGTGTGTGTGTGTG 517

Qy        343 TGTGTGTGTGTATGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTA 402
              |||||||||| |||||||||| |     |           |||| || ||| ||||||
Db        518 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCTNNNNNTTTTTTTTTTTTTTTTTT 577

Qy        403 TTTATTTATTTTTT 416
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Db        578 TTTTTTNTTTTTTT 591
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RESULT 12
AG429109
LOCUS AG429109 766 bp DNA linear GSS 03-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-303I17.T7, genomic survey sequence.
ACCESSION AG429109
VERSION AG429109.1 GI:48072172
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 766)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
source 1. .766
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
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/clone="MSMg01-303I17.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

Query Match 9.2%; Score 57.6; DB 9; Length 766;
Best Local Similarity 61.8%; Pred. No. 0.028;
Matches 81; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Qy        287 CTTTCAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTG 346
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Qy        347 TGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTA 406
              ||||||| |||||||||| |                ||||  || ||| |||||| |||
Db        213 TGTGTGTGTGTGTGTGTGTGTGTNNNNNNNNNTTTTNTTTTTTTTTTTTTTTTTTTTTTT 272

Qy        407 TTTATTTTTG 417
              ||| | | |||
Db        273 TTTTTNTCTTG 283
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RESULT 13
AG602238
LOCUS AG602238 735 bp DNA linear GSS 05-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-534J10.T7, genomic survey sequence.
ACCESSION AG602238
VERSION AG602238.1 GI:48363068
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 735)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
source 1. .735
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/sub_species="molossinus"
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/clone="MSMg01-534J10.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

Query Match 9.1%; Score 57.4; DB 9; Length 735;
Best Local Similarity 53.9%; Pred. No. 0.031;
Matches 97; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

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Qy        237 TTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTC 296
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Db        269 TTGGGTTTTATATGCACTAGACAAATACTTCCATCTTAGCTACATCTCATTTCTGGACTG 328

Qy        297 TAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTGTATG 356
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Db        329 GAACACTTTTCAGAAAATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 388

Qy        357 TGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTT 416
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Db        389 TGTGTGTGTGTGTGNNNNNNNNNNNTTNNNTTTTTTTTTTTTNNNTTTTTTTTTTTTTT 448
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RESULT 14
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LOCUS AG604663 802 bp DNA linear GSS 05-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-537M08.TJ, genomic survey sequence.
ACCESSION AG604663
VERSION AG604663.1 GI:48365493
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

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  TITLE     BAC end Sequences of Library MSMg01
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 802)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : TJ
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             9.1%;  Score 57.4;  DB 9;  Length 802;
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  Matches   64;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy        327 TGTGCGTGCGTGCGTGTGTGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTT 386
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Db        365 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTNTNNNNNNNNNNNNNNNTTTT 424

Qy        387 TATTATTTATTTTTTATTTATTTATTTTTTG 417
              | || ||| |||||| ||| ||| |||||||
Db        425 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTG 455


RESULT 15
AG591362
LOCUS       AG591362                743 bp    DNA     linear   GSS 05-JUN-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-520E18.T7, genomic survey
            sequence.
ACCESSION   AG591362
VERSION     AG591362.1  GI:48352192
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     BAC end Sequences of Library MSMg01
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 743)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
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                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             9.1%;  Score 57;  DB 9;  Length 743;
  Best Local Similarity   70.0%;  Pred. No. 0.038;
  Matches   63;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy        327 TGTGCGTGCGTGCGTGTGTGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTT 386
              |||| ||| ||| |||||||||||||| |||||||||| |                 |||
Db        647 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTNNNNNNNNNNNNNNNTTT 706

Qy        387 TATTATTTATTTTTTATTTATTTATTTTTT 416
              | || ||| |||||| ||| ||| ||||||
Db        707 TTTTNTTTTTTTTTTTTTTTTTTTTTTTT 736


Search completed: April 26, 2005, 20:13:36
Job time : 2677.73 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 15:59:17 ; Search time 430.989 Seconds
(without alignments)
8625.744 Million cell updates/sec

Title: US-09-601-267-37
Perfect score: 628
Sequence: 1 tgtgaccttgaactacagac.....ttctcgctgacttccagcgg 628

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	628	100.0	4044	2	AAZ07248	Aaz07248 Mouse tel
	3	575.8	91.7	622	2	AAZ07322	Aaz07322 Mouse tel
	4	344.4	54.8	1259	2	AAT11026	Aat11026 DNA encod
	5	137	21.8	560	2	AAT85372	Aat85372 Mouse tel
	6	135.4	21.6	534	2	AAT11025	Aat11025 Mouse tel
	7	79	12.6	397	13	ADT86993	Adt86993 Mouse tel
	8	71.8	11.4	568	2	AAT11030	Aat11030 DNA encod
	9	65.8	10.5	552	2	AAT11029	Aat11029 DNA encod
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	11	60.2	9.6	6731	13	ADS89732	Ads89732 Oligonucl
	12	60.2	9.6	9731	6	ABL32991	Abl32991 Human imm
	13	55.2	8.8	7135	4	AAS46424	Aas46424 Tumour su
c	14	54.6	8.7	599	5	ABV18162	Abv18162 Human pro
c	15	54.6	8.7	629	5	ABV47950	Abv47950 Human pro
	16	54.6	8.7	43572	12	ADQ97861	Adq97861 Mouse can
c	17	54.4	8.7	171324	11	ACN43892	Acn43892 Mouse gen
	18	54	8.6	6988	6	ABL34441	Abl34441 Human imm
	19	52.8	8.4	11691	6	ABL34240	Abl34240 Human imm
	20	52.6	8.4	6306	4	AAK85746	Aak85746 Human imm
	21	52.4	8.3	8961	6	ABK28428	Abk28428 DNA trans
	22	52.4	8.3	8961	6	ABL49380	Abl49380 Human pol
c	23	52.4	8.3	219352	13	ABD33098	Abd33098 Murine ca
c	24	52.2	8.3	85341	13	ABD32883	Abd32883 Human can
	25	52	8.3	7304	5	ABA17950	Aba17950 Human ner
	26	52	8.3	7306	5	ABA17949	Aba17949 Human ner
	27	52	8.3	9177	5	ABA17951	Aba17951 Human ner
	28	51.8	8.2	7104	6	ABL34588	Abl34588 Human met
	29	51.8	8.2	7104	6	ABL70395	Abl70395 Chemicall
	30	51.8	8.2	7104	7	ADS99849	Ads99849 Bisulphit
c	31	51.6	8.2	433	4	AAI87368	Aai87368 Human pol
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	36	50.8	8.1	17594	6	ABL34027	Abl34027 Human imm
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	38	50.6	8.1	42104	11	ACN44606	Acn44606 Human gen
c	39	50.4	8.0	415	4	AAI85215	Aai85215 Human pol
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	41	50.4	8.0	5274	12	ADQ25455	Adq25455 Human sof
c	42	50.4	8.0	9950	8	ABX17768	Abx17768 DNA encod
	43	50.4	8.0	48853	13	ABD33472	Abd33472 Murine ca
c	44	50.4	8.0	110000	10	ABQ84281_3	Continuation (4 of
	45	50.2	8.0	2983	4	AAK83652	Aak83652 Human imm

ALIGNMENTS

RESULT 1
AAZ07249
ID AAZ07249 standard; DNA; 628 BP.
XX
AC AAZ07249;
XX
DT 22-OCT-1999 (first entry)
XX
DE Mouse telomerase RNA gene (terc) 5' flanking region.
XX
KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; terc;
KW gene therapy; thymidine kinase gene; anticancer therapy; mouse; ss.
XX
OS Mus sp.
XX
PN WO9938964-A2.
XX
PD 05-AUG-1999.
XX
PF 29-JAN-1999; 99WO-GB000308.
XX
PR 29-JAN-1998; 98GB-00001902.
XX
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI Keith WN;
XX
DR WPI; 1999-479183/40.
XX
PT Mouse and human telomerase RNA gene promoters, useful for tumor specific
PT gene therapy.
XX
PS Claim 9; Fig 4b; 109pp; English.
XX
CC The invention relates to promoter regions from mouse and human telomerase
CC RNA (TR) component genes. The TR gene promoter can be linked to a
CC heterologous gene, especially a gene encoding a cytotoxin, for therapy of
CC cancer, especially neoplasias. The telomerase is necessary for the
CC unrestricted proliferative capacity of many human cancers. Mutation or
CC dysregulation of the telomerase repression pathway may cause reactivation
CC or upregulation of telomerase expression in cancer. Substances,
CC identified in the methods, can be used to block transcription from the TR
CC gene promoter through interaction of the 5' regulatory sequences. These

```
CC   substances, e.g. antisense oligonucleotides, transcription factors,
CC   peptide nucleic acids and factors that disrupt signal transduction, are
CC   useful for cancer therapy. In particular, gene therapy vectors
CC   (especially pGT62-codAupp) comprising the promoter and a viral thymidine
CC   kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
CC   neoplasia can be controlled or treated. Direct down-regulation of
CC   telomerase RNA gene through manipulation of transcription factors may be
CC   effective anticancer therapy and the cloning of the hTR gene promoter
CC   allows the analysis of therapeutic molecules which modulate hTR promoter
CC   activity. The present sequence represents a mouse TR gene (terc) 5'
CC   flanking sequence
XX
SQ   Sequence 628 BP; 129 A; 137 C; 160 G; 202 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 628;  DB 2;  Length 628;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-144;
  Matches  628;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 60

Qy         61 GGTCAGCTACCCTTGAAATCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCACT 120
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Db         61 GGTCAGCTACCCTTGAAATCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCACT 120

Qy        121 CACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCGCCACTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 TTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTTT 240
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Db        181 TTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTTT 240

Qy        241 TTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAGT 300

Qy        301 ATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTGTATGTGTG 360
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Db        301 ATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTATGTGTG 360

Qy        361 TGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCAA 420

Qy        421 GTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCCG 480

Qy        481 CAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCTA 540

Qy        541 GGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCC 600

Qy        601 CGCTGTTTTTCTCGCTGACTTCCAGCGG 628
              |||||||||||||||||||||||||||||
Db        601 CGCTGTTTTTCTCGCTGACTTCCAGCGG 628


RESULT 2
AAZ07248
ID   AAZ07248 standard; DNA; 4044 BP.
XX
AC   AAZ07248;
XX
DT   22-OCT-1999  (first entry)
XX
DE   Mouse telomerase RNA gene (terc) sequence.
XX
KW   Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; terc;
KW   gene therapy; thymidine kinase gene; anticancer therapy; mouse; ss.
XX
OS   Mus sp.
XX
PN   WO9938964-A2.
XX
PD   05-AUG-1999.
XX
PF   29-JAN-1999;   99WO-GB000308.
XX
PR   29-JAN-1998;   98GB-00001902.
XX
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Keith WN;
XX
DR   WPI; 1999-479183/40.
XX
PT   Mouse and human telomerase RNA gene promoters, useful for tumor specific
PT   gene therapy.
XX
PS   Disclosure; Fig 2; 109pp; English.
XX
CC   The invention relates to promoter regions from mouse and human telomerase
CC   RNA (TR) component genes. The TR gene promoter can be linked to a
CC   heterologous gene, especially a gene encoding a cytotoxin, for therapy of
CC   cancer, especially neoplasias. The telomerase is necessary for the
CC   unrestricted proliferative capacity of many human cancers. Mutation or
CC   dysregulation of the telomerase repression pathway may cause reactivation
CC   or upregulation of telomerase expression in cancer. Substances,
CC   identified in the methods, can be used to block transcription from the TR
CC   gene promoter through interaction of the 5' regulatory sequences. These
CC   substances, e.g. antisense oligonucleotides, transcription factors,
CC   peptide nucleic acids and factors that disrupt signal transduction, are
CC   useful for cancer therapy. In particular, gene therapy vectors
CC   (especially pGT62-codAupp) comprising the promoter and a viral thymidine
CC   kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
CC   neoplasia can be controlled or treated. Direct down-regulation of
CC   telomerase RNA gene through manipulation of transcription factors may be
CC   effective anticancer therapy and the cloning of the hTR gene promoter
CC   allows the analysis of therapeutic molecules which modulate hTR promoter
CC   activity. The present sequence represents a mouse TR gene (terc) sequence
XX
SQ   Sequence 4044 BP; 1023 A; 928 C; 973 G; 1120 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 628;  DB 2;  Length 4044;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-144;
  Matches  628;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1010 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 1069

Qy         61 GGTCAGCTACCCTTGAAATCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCACT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 GGTCAGCTACCCTTGAAATCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCACT 1129

Qy        121 CACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCGCCACTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1130 CACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCGCCACTT 1189

Qy        181 TTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1190 TTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTTT 1249

Qy        241 TTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1250 TTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAGT 1309

Qy        301 ATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTGTATGTGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1310 ATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTGTATGTGTG 1369
```

```
Qy        361 TGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1370 TGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCAA 1429

Qy        421 GTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1430 GTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCCG 1489

Qy        481 CAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1490 CAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCTA 1549

Qy        541 GGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1550 GGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCC 1609

Qy        601 CGCTGTTTTTCTCGCTGACTTCCAGCGG 628
              |||||||||||||||||||||||||||||
Db       1610 CGCTGTTTTTCTCGCTGACTTCCAGCGG 1637
```

RESULT 3
AAZ07322
ID AAZ07322 standard; DNA; 622 BP.
XX
AC AAZ07322;
XX
DT 22-OCT-1999 (first entry)
XX
DE Mouse telomerase RNA gene (terc) promoter from Balb/c clones.
XX
KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; terc;
KW gene therapy; thymidine kinase gene; anticancer therapy; mouse; ss.
XX
OS Mus sp.
XX
PN WO9938964-A2.
XX
PD 05-AUG-1999.
XX
PF 29-JAN-1999; 99WO-GB000308.
XX
PR 29-JAN-1998; 98GB-00001902.
XX
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI Keith WN;
XX
DR WPI; 1999-479183/40.
XX
PT Mouse and human telomerase RNA gene promoters, useful for tumor specific
PT gene therapy.
XX
PS Disclosure; Fig 9; 109pp; English.
XX
CC The invention relates to promoter regions from mouse and human telomerase
CC RNA (TR) component genes. The TR gene promoter can be linked to a
CC heterologous gene, especially a gene encoding a cytotoxin, for therapy of
CC cancer, especially neoplasias. The telomerase is necessary for the
CC unrestricted proliferative capacity of many human cancers. Mutation or
CC dysregulation of the telomerase repression pathway may cause reactivation
CC or upregulation of telomerase expression in cancer. Substances,
CC identified in the methods, can be used to block transcription from the TR
CC gene promoter through interaction of the 5' regulatory sequences. These
CC substances, e.g. antisense oligonucleotides, transcription factors,
CC peptide nucleic acids and factors that disrupt signal transduction, are
CC useful for cancer therapy. In particular, gene therapy vectors
CC (especially pGT62-codAupp) comprising the promoter and a viral thymidine
CC kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
CC neoplasia can be controlled or treated. Direct down-regulation of
CC telomerase RNA gene through manipulation of transcription factors may be
CC effective anticancer therapy and the cloning of the hTR gene promoter
CC allows the analysis of therapeutic molecules which modulate hTR promoter
CC activity. The present sequence represents a mouse TR gene promoter
CC sequence from balb/c clones. Sequence analysis shows that this sequence
CC is identical to the terc gene promoter sequence shown in AAZ07249 apart
CC from minor polymorphisms
XX
SQ Sequence 622 BP; 131 A; 136 C; 159 G; 196 T; 0 U; 0 Other;

```
  Query Match             91.7%;  Score 575.8;  DB 2;  Length 622;
  Best Local Similarity   98.1%;  Pred. No. 8.5e-132;
  Matches  617;  Conservative    0;  Mismatches    2;  Indels   10;  Gaps    3;

Qy          1 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 61

Qy         61 GGTCAGCTACCCTTGAAA-TCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCAC 119
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         62 GGTCAGCTACCCTTGAAATTCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCAC 121

Qy        120 TCACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCGCCACT 179
              |||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        122 TCACAAGAGATCCGCCTGCCTTCTG----TCAAATTCTGGAATTAAAGATTTGCGCCACT 177

Qy        180 TTTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTT 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||    ||||
Db        178 TTTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAA-----TTTT 232

Qy        240 TTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAG 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 TTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAG 292

Qy        300 TATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTATGTGT 359
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        293 TATATTTCAGAAACCAAGCCTCAGAAATGTGCGTGCGTGCGTGTGTGTGTGTATGTGT 352

Qy        360 GTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCA 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 GTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCA 412

Qy        420 AGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCC 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 AGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCC 472

Qy        480 GCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCT 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 GCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCT 532

Qy        540 AGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGC 599
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        533 AGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTCGTTCTCCGC 592

Qy        600 CCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
              |||||||||||||||||||||||||||||
Db        593 CCGCTGTTTTTCTCGCTGACTTCCAGCGG 621
```

RESULT 4
AAT11026
ID AAT11026 standard; DNA; 1259 BP.
XX
AC AAT11026;
XX
DT 09-JUN-1996 (first entry)
XX
DE DNA encoding the mouse telomerase RNA component.
XX
KW Telomerase; mammal; antisense; triplex forming oligonucleotide; plasmid;
KW probe; primer; ribozyme; ss.
XX
OS Mus musculus.
XX
PN WO9601614-A2.

```
XX
PD   25-JAN-1996.
XX
PF   07-JUL-1995;   95WO-US008620.
XX
PR   07-JUL-1994;   94US-00272102.
PR   27-OCT-1994;   94US-00330123.
PR   13-FEB-1995;   95US-00387524.
PR   07-JUN-1995;   95US-00485778.
XX
PA   (COLD-) COLD SPRING HARBOR LAB.
PA   (GERO-) GERON CORP.
XX
PI   Andrews WH,  Avillon AA,  Feng J,  Funk W,  Greider C,  Marhuenda MA;
PI   Villeponteau B;
XX
DR   WPI; 1996-097428/10.
XX
PT   RNA components of (non)human mammalian telomerase(s) - useful in studying
PT   cell senescence and immortalisation.
XX
PS   Claim 11; Fig 3; 85pp; English.
XX
CC   The RNA components of (non) human mammalian telomerase(s) especially from
CC   mouse, rat and chinese hamster are all claimed. Antisense
CC   oligonucleotides can be used to block the activity of the telomerase;
CC   probes and primers can be used in detection; vectors and host cells
CC   transformed with the isolated telomerase genes can be used for production
CC   of telomerases; RNA and DNA ribozymes and triplex forming
CC   oligonucleotides directed against the telomerase genes can be used
CC   therapeutically as can plasmids. A mouse which lacks the telomerase gene
CC   (also claimed) can be used for study of telomere regulation in vivo, and
CC   the role it plays in immortalisation. This DNA sequence encodes the mouse
CC   telomerase RNA component
XX
SQ   Sequence 1259 BP; 265 A; 312 C; 369 G; 313 T; 0 U; 0 Other;

  Query Match             54.8%;  Score 344.4;  DB 2;  Length 1259;
  Best Local Similarity   99.7%;  Pred. No. 9.9e-75;
  Matches  345;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        283 CCTACTTTCAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTG 342
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 CCTACTTTCAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTG 382

Qy        343 TGTGTGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTA 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TGTGTGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTA 442

Qy        403 TTTATTTATTTTTTGCAAGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGG 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TTTATTTATTTTTTGCAAGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGG 502

Qy        463 GAAGAGGGAGCATTTCCGCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATT 522
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        503 GAAGAGGGAGCATTTCCGCAAGTGCTGGGCTCGACCAATCAGCGCGAGCCATGGGGTATT 562

Qy        523 TAAGGTCGAGGGCGGCTAGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCT 582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TAAGGTCGAGGGCGGCTAGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCT 622

Qy        583 GGTCTTTTGTTCTCCGCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        623 GGTCTTTTGTTCTCCGCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 668


RESULT 5
AAT85372
ID   AAT85372 standard; DNA; 560 BP.
XX
AC   AAT85372;
XX
DT   15-APR-1998  (first entry)
XX
DE   Mouse telomerase RNA component gene.
XX
KW   Telomerase gene; transgenic organism; carcinogen; neoplastic growth;
KW   cell growth; cell senescence; mouse; ss.
XX
OS   Mus sp.
XX
PN   WO9735967-A2.
XX
PD   02-OCT-1997.
XX
PF   21-MAR-1997;   97WO-US005070.
XX
PR   28-MAR-1996;   96US-00623166.
XX
PA   (COLD-) COLD SPRING HARBOR LAB.
PA   (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI   Greider C,  Marhuenda MA,  Depinho RA,  Lee H;
XX
DR   WPI; 1997-489631/45.
XX
PT   Non-human transgenic animal not expressing endogenous telomerase - useful
PT   to test the carcinogenicity of a test compound, or to study cell growth,
PT   division or senescence.
XX
PS   Disclosure; Fig 6; 58pp; English.
XX
CC   This sequence represents the mouse telomerase RNA component gene. This
CC   sequence can be used in the transgenic organism of the invention. The
CC   organism is a non-human transgenic organism in which at least one
CC   endogenous telomerase gene encoding a telomerase component is altered and
CC   telomerase activity is altered or is not expressed. The transgenic
CC   organisms can be used as models to study telomerase activity. They can
CC   also be used as a system to test compounds suspected of being
CC   carcinogenic by exposing animals to the compound and determining
CC   neoplastic growth as an indicator of carcinogenicity. The cells and
CC   derived tissues are used to study cell growth and division and cell
CC   senescence. The organisms are able to produce cells and tissues that, in
CC   their wild type form, cannot be easily studied in vitro due to undergoing
CC   small numbers of cell divisions
XX
SQ   Sequence 560 BP; 90 A; 183 C; 188 G; 99 T; 0 U; 0 Other;

  Query Match             21.8%;  Score 137;  DB 2;  Length 560;
  Best Local Similarity   100.0%;  Pred. No. 9e-24;
  Matches  137;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        492 CTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCTAGGCCTCGGCAC 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCTAGGCCTCGGCAC 60

Qy        552 CTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTTTC 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTTTC 120

Qy        612 TCGCTGACTTCCAGCGG 628
              |||||||||||||||||
Db        121 TCGCTGACTTCCAGCGG 137


RESULT 6
AAT11025
ID   AAT11025 standard; DNA; 534 BP.
XX
AC   AAT11025;
XX
DT   09-JUN-1996  (first entry)
XX
DE   Mouse telomerase RNA component.
XX
KW   Telomerase; mammal; antisense; triplex forming oligonucleotide; plasmid;
```

KW probe; primer; ribozyme; ss.
XX
OS Mus musculus.
XX
PN WO9601614-A2.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95WO-US008620.
XX
PR 07-JUL-1994; 94US-00272102.
PR 27-OCT-1994; 94US-00330123.
PR 13-FEB-1995; 95US-00387524.
PR 07-JUN-1995; 95US-00485778.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (GERO-) GERON CORP.
XX
PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C, Marhuenda MA;
PI Villeponteau B;
XX
DR WPI; 1996-097428/10.
XX
PT RNA components of (non)human mammalian telomerase(s) - useful in studying
PT cell senescence and immortalisation.
XX
PS Claim 2; Fig 4; 85pp; English.
XX
CC The RNA components of (non) human mammalian telomerase(s) especially from
CC mouse, rat and chinese hamster are all claimed. Antisense
CC oligonucleotides can be used to block the activity of the telomerase;
CC probes and primers can be used in detection; vectors and host cells
CC transformed with the isolated telomerase genes can be used for production
CC of telomerases; RNA and DNA ribozymes and triplex forming
CC oligonucleotides directed against the telomerase genes can be used
CC therapeutically as can plasmids. A mouse which lacks the telomerase gene
CC (also claimed) can be used for study of telomere regulation in vivo, and
CC the role it plays in immortalisation. This is the mouse telomerase RNA
CC component
XX
SQ Sequence 534 BP; 84 A; 169 C; 184 G; 0 T; 97 U; 0 Other;

Query Match 21.6%; Score 135.4; DB 2; Length 534;
Best Local Similarity 69.3%; Pred. No. 2.2e-23;
Matches 95; Conservative 41; Mismatches 1; Indels 0; Gaps 0;

```
Qy        492 CTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCTAGGCCTCGGCAC 551
              |:|||||||:|||||| ||||:||||:|:::||||:||||||||||:|||||:||||||
Db          1 CUCGACCAAUCAGCGCGAGCCAUGGGGUAUUUAAGGUCGAGGGCGGCUAGGCCUCGGCAC 60

Qy        552 CTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTTTC 611
              |:|||||:||::::||::|||:|:||||::|:||:|::::|::|:|||||||:|:::::|
Db         61 CUAACCCUGAUUUUCAUUAGCUGUGGGUUCUGGUCUUUUGUUCUCCGCCCGCUGUUUUUC 120

Qy        612 TCGCTGACTTCCAGCGG 628
              :|||:|||::|||||||
Db        121 UCGCUGACUUCCAGCGG 137
```

RESULT 7
ADT86993
ID ADT86993 standard; DNA; 397 BP.
XX
AC ADT86993;
XX
DT 16-DEC-2004 (first entry)
XX
DE Mouse telomerase RNA (TER) derived DNA.
XX
KW ds; snoRNA; small nuclear RNA; box H/ACA; mRNA splicing; mRNA processing;
KW rRNA processing; RNA methylation site selection; pseudouridine formation;
KW H/ACA-snoRNA; telomerase RNA; cancer; tumour; cell proliferation;
KW trypanosome infection; RNAi-mediated degradation; 26556; neo gene; siRNA;
KW small interfering RNA; telomerase RNA; TER; mouse; selection marker.
XX
OS Mus musculus.
XX
PN WO2004069148-A2.
XX
PD 19-AUG-2004.
XX
PF 04-FEB-2004; 2004WO-IL000108.
XX
PR 04-FEB-2003; 2003US-0444670P.
XX
PA (UYBA-) UNIV BAR-ILAN.
XX
PI Michaeli S;
XX
DR WPI; 2004-604326/58.
XX
PT New isolated small nuclear RNA (snoRNA) polynucleotides, useful for
PT inducing RNAi-mediated degradation of snoRNA or for treating diseases
PT associated with activity of small nuclear RNA, e.g. cancer.
XX
PS Disclosure; SEQ ID NO 40; 79pp; English.
XX
CC The present invention provides the method for downregulating snoRNA
CC (small nuclear RNA) molecules or the box H/ACA containing RNA molecules.
CC The method can be used to treat the diseases associated with the activity
CC of small nuclear RNA. Small nuclear RNA molecules are the important
CC regulators of gene expression. They participate in mRNA splicing, mRNA
CC and rRNA processing, RNA methylation site selection and pseudouridine
CC formation (box H/ACA-snoRNA). The telomerase RNA is an important nuclear
CC RNA which serves as a template for telomerase replication. It contains
CC box H/ACA like domain which confers the functional localisation of this
CC RNA to the nucleus. The majority of the cancerous tumours contain active
CC telomerase which contributes to cell proliferation. It has been found
CC that the trypanosome infection is associated with the parasite's snoRNA
CC expression. The polynucleotides of the invention are useful for inducing
CC RNAi-mediated degradation of a small nuclear RNA. They are useful for
CC down regulating snoRNA molecules or box H/ACA-containing RNA molecules.
CC The telomerase activity of the cancer cells can be inhibited by a
CC polynucleotide sequence which is capable of inducing RNAi mediated
CC degradation of the human telomerase RNA. The snoRNA-2 was found to be
CC part of a gene cluster which includes two additional coding sequences of
CC novel RNA termed as h2 and h3. It has also observed that the snoRNA-2
CC silencing occurs at the mature RNA transcript level and snoRNA silencing
CC results in decreased snoRNA-2 guided methylation on the 5.8rRNA. The
CC expression level of the snoRNA-2 transcripts depend on the orientation of
CC the snoRNA-2 gene with respect to neo gene (selection marker). It has
CC also found that the silencing of sno-RNA-2 is mediated through the
CC production of siRNA (small interfering RNA) which can produce in both
CC nucleus and cytoplasm. The invention suggests that the siRNA mediated
CC snoRNA-2 silencing is not unique to snoRNA cluster-2. It is also
CC applicable for mammalian snoRNAs. The proposed nucleic acid construct
CC comprises of a selection marker gene in reverse orientation. It also
CC includes two promoters and each promoter is capable of directing the
CC transcription of a specific strand of the nucleotide. The presented
CC nucleotide sequence is the mouse telomerase RNA (TER) derived DNA.
XX
SQ Sequence 397 BP; 59 A; 136 C; 129 G; 73 T; 0 U; 0 Other;

Query Match 12.6%; Score 79; DB 13; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        550 ACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTT 609
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTT 60

Qy        610 TCTCGCTGACTTCCAGCGG 628
              ||||||||||||||||||||
Db         61 TCTCGCTGACTTCCAGCGG 79
```

```
RESULT 8
AAT11030
ID   AAT11030 standard; DNA; 568 BP.
XX
AC   AAT11030;
XX
DT   09-JUN-1996  (first entry)
XX
DE   DNA encoding the rat telomerase RNA component.
XX
KW   Telomerase; mammal; antisense; triplex forming oligonucleotide; plasmid;
KW   probe; primer; ribozyme; ss.
XX
OS   Rattus rattus.
XX
PN   WO9601614-A2.
XX
PD   25-JAN-1996.
XX
PF   07-JUL-1995;   95WO-US008620.
XX
PR   07-JUL-1994;   94US-00272102.
PR   27-OCT-1994;   94US-00330123.
PR   13-FEB-1995;   95US-00387524.
PR   07-JUN-1995;   95US-00485778.
XX
PA   (COLD-) COLD SPRING HARBOR LAB.
PA   (GERO-) GERON CORP.
XX
PI   Andrews WH,  Avillon AA,  Feng J,  Funk W,  Greider C,  Marhuenda MA;
PI   Villeponteau B;
XX
DR   WPI; 1996-097428/10.
XX
PT   RNA components of (non)human mammalian telomerase(s) - useful in studying
PT   cell senescence and immortalisation.
XX
PS   Claim 36; Fig 7; 85pp; English.
XX
CC   The RNA components of (non) human mammalian telomerase(s) especially from
CC   mouse, rat and chinese hamster are all claimed. Antisense
CC   oligonucleotides can be used to block the activity of the telomerase;
CC   probes and primers can be used in detection; vectors and host cells
CC   transformed with the isolated telomerase genes can be used for production
CC   of telomerases; RNA and DNA ribozymes and triplex forming
CC   oligonucleotides directed against the telomerase genes can be used
CC   therapeutically as can plasmids. A mouse which lacks the telomerase gene
CC   (also claimed) can be used for study of telomere regulation in vivo, and
CC   the role it plays in immortalisation. This DNA sequence encodes the rat
CC   telomerase RNA component
XX
SQ   Sequence 568 BP; 100 A; 160 C; 187 G; 121 T; 0 U; 0 Other;

  Query Match            11.4%;  Score 71.8;  DB 2;  Length 568;
  Best Local Similarity   83.2%;  Pred. No. 1e-07;
  Matches   94;  Conservative    0;  Mismatches   17;  Indels    2;  Gaps    1;

Qy        516 GGGTATTTAAGGTCGAGGGCGGCTAGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGT 575
              ||||||||| || | ||||| ||  | | || ||  ||||||||  | ||   |||||||
Db         51 GGGTATTTAGGGACAAGGGCCGCGCGACTTCTGCGTCTAACCCTATTGTT--ATAGCTGT 108

Qy        576 GGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
              |||||||| ||||||||||||||||||||||||||||||||||||||| ||||||
Db        109 GGGTTCTGTTCTTTTGTTCTCCGCCCGCTGTTTTTCTCGCTGACTTTCAGCGG 161


RESULT 9
AAT11029
ID   AAT11029 standard; DNA; 552 BP.
XX
AC   AAT11029;
XX
DT   09-JUN-1996  (first entry)
XX
DE   DNA encoding the chinese hamster telomerase RNA component.
XX
KW   Telomerase; mammal; antisense; triplex forming oligonucleotide; plasmid;
KW   probe; primer; ribozyme; ss.
XX
OS   Cricetulus griseus.
XX
PN   WO9601614-A2.
XX
PD   25-JAN-1996.
XX
PF   07-JUL-1995;   95WO-US008620.
XX
PR   07-JUL-1994;   94US-00272102.
PR   27-OCT-1994;   94US-00330123.
PR   13-FEB-1995;   95US-00387524.
PR   07-JUN-1995;   95US-00485778.
XX
PA   (COLD-) COLD SPRING HARBOR LAB.
PA   (GERO-) GERON CORP.
XX
PI   Andrews WH,  Avillon AA,  Feng J,  Funk W,  Greider C,  Marhuenda MA;
PI   Villeponteau B;
XX
DR   WPI; 1996-097428/10.
XX
PT   RNA components of (non)human mammalian telomerase(s) - useful in studying
PT   cell senescence and immortalisation.
XX
PS   Claim 46; Fig 7; 85pp; English.
XX
CC   The RNA components of (non) human mammalian telomerase(s) especially from
CC   mouse, rat and chinese hamster are all claimed. Antisense
CC   oligonucleotides can be used to block the activity of the telomerase;
CC   probes and primers can be used in detection; vectors and host cells
CC   transformed with the isolated telomerase genes can be used for production
CC   of telomerases; RNA and DNA ribozymes and triplex forming
CC   oligonucleotides directed against the telomerase genes can be used
CC   therapeutically as can plasmids. A mouse which lacks the telomerase gene
CC   (also claimed) can be used for study of telomere regulation in vivo, and
CC   the role it plays in immortalisation. This DNA sequence encodes the
CC   chinese hamster telomerase RNA component
XX
SQ   Sequence 552 BP; 97 A; 182 C; 184 G; 89 T; 0 U; 0 Other;

  Query Match            10.5%;  Score 65.8;  DB 2;  Length 552;
  Best Local Similarity   73.5%;  Pred. No. 3e-06;
  Matches  111;  Conservative    0;  Mismatches   37;  Indels    3;  Gaps    2;

Qy        480 GCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCA--TGGGGTATTTAAGGTCGAGGGCGG 537
              || || || ||   || ||||||||||||||||    ||||| |||||| |||     |
Db          1 GCGAGAGCCGGCGCCGGCCAATCAGCGCGCGCCACCCCGGGTACTTAAGGGCGACCTGGC 60

Qy        538 CTAGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCC 597
              | ||      |||||||||| ||     |||||||||| |||  |||| | |||||
Db         61 GGGCGGCTGCCAGTCTAACCCTGAATTCTGAGAGCTGTGGGTACTGTGCTTTCG-TCTCC 119

Qy        598 GCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
              |||||||||||||||||||||||||||||||
Db        120 GCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 150


RESULT 10
ADS89458
ID   ADS89458 standard; DNA; 6731 BP.
XX
AC   ADS89458;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Oligonucleotide of the invention SEQ ID NO:474.
XX
```

KW ss; cell proliferative disorder; breast; methylation; cytostatic;
KW gene therapy; single nucleotide polymorphism; SNP.
XX
OS Unidentified.
XX
PN WO2004035803-A2.
XX
PD 29-APR-2004.
XX
PF 01-OCT-2003; 2003WO-EP010881.
XX
PR 01-OCT-2002; 2002DE-01045779.
PR 07-JAN-2003; 2003DE-01000096.
PR 17-APR-2003; 2003DE-01017955.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
XX
DR WPI; 2004-348468/32.
XX
PT Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject.
XX
PS Disclosure; SEQ ID NO 474; 104pp; English.
XX
CC The invention relates to a novel method for predicting the responsiveness
CC of a subject with a cell proliferative disorder of the breast tissues to
CC a therapy comprising analysing the methylation pattern of a target
CC nucleic acid by contacting at least one of the target nucleic acids in a
CC biological sample obtained from the subject prior to or during treatment.
CC The method of the invention has cytostatic activity, and may have a use
CC in gene therapy. The set of oligonucleotides comprising at least two of
CC the oligomers are useful for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC methods, nucleic acid, oligonucleotide, and kit are useful for the
CC treatment, characterisation, classification and/or differentiation, of
CC breast cell proliferative disorders. The method is also useful for
CC predicting the responsiveness of a subject with a cell proliferative
CC disorder of the breast tissues to a therapy. The present sequence is used
CC in the exemplification of the invention.
XX
SQ Sequence 6731 BP; 2098 A; 49 C; 1358 G; 3226 T; 0 U; 0 Other;

Query Match 9.6%; Score 60.2; DB 13; Length 6731;
Best Local Similarity 57.8%; Pred. No. 0.00015;
Matches 107; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 231 TTTTTTTTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTT 290
Db 5456 TTATTGTTTTTTTTTTATTTTATTATTTTGGGAGAAGGGTATTTGGGGGGTAAATAATTT 5515

Qy 291 CAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTG 350
Db 5516 TTTTGTTGTTTGAATTTTTTATATAATTTAAATTTGTGTGTGTGTGTGTGTGTGTGTG 5575

Qy 351 TGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTA 410
Db 5576 TGTGTGTGTGTGTGTATGATAGAGGGAGTTTGTGTGTTAGAGTGTGTTTTTTTTTTTGA 5635

Qy 411 TTTTT 415
Db 5636 TTTTT 5640

RESULT 11
ADS89732
ID ADS89732 standard; DNA; 6731 BP.
XX
AC ADS89732;
XX
DT 18-NOV-2004 (first entry)
XX
DE Oligonucleotide of the invention SEQ ID NO:748.
XX
KW ss; cell proliferative disorder; breast; methylation; cytostatic;
KW gene therapy; single nucleotide polymorphism; SNP.
XX
OS Unidentified.
XX
PN WO2004035803-A2.
XX
PD 29-APR-2004.
XX
PF 01-OCT-2003; 2003WO-EP010881.
XX
PR 01-OCT-2002; 2002DE-01045779.
PR 07-JAN-2003; 2003DE-01000096.
PR 17-APR-2003; 2003DE-01017955.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
XX
DR WPI; 2004-348468/32.
XX
PT Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject.
XX
PS Disclosure; SEQ ID NO 748; 104pp; English.
XX
CC The invention relates to a novel method for predicting the responsiveness
CC of a subject with a cell proliferative disorder of the breast tissues to
CC a therapy comprising analysing the methylation pattern of a target
CC nucleic acid by contacting at least one of the target nucleic acids in a
CC biological sample obtained from the subject prior to or during treatment.
CC The method of the invention has cytostatic activity, and may have a use
CC in gene therapy. The set of oligonucleotides comprising at least two of
CC the oligomers are useful for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC methods, nucleic acid, oligonucleotide, and kit are useful for the
CC treatment, characterisation, classification and/or differentiation, of
CC breast cell proliferative disorders. The method is also useful for
CC predicting the responsiveness of a subject with a cell proliferative
CC disorder of the breast tissues to a therapy. The present sequence is used
CC in the exemplification of the invention.
XX
SQ Sequence 6731 BP; 2098 A; 0 C; 1358 G; 3275 T; 0 U; 0 Other;

Query Match 9.6%; Score 60.2; DB 13; Length 6731;
Best Local Similarity 57.8%; Pred. No. 0.00015;
Matches 107; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 231 TTTTTTTTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTT 290
Db 5456 TTATTGTTTTTTTTTTATTTTATTATTTTGGGAGAAGGGTATTTGGGGGGTAAATAATTT 5515

Qy 291 CAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTG 350
Db 5516 TTTTGTTGTTTGAATTTTTTATATAATTTAAATTTGTGTGTGTGTGTGTGTGTGTGTG 5575

Qy 351 TGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTA 410
Db 5576 TGTGTGTGTGTGTGTATGATAGAGGGAGTTTGTGTGTTAGAGTGTGTTTTTTTTTTTGA 5635

Qy 411 TTTTT 415
Db 5636 TTTTT 5640

RESULT 12
ABL32991
ID ABL32991 standard; DNA; 9731 BP.
XX
AC ABL32991;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 964.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
PS Claim 1; SEQ ID NO 964; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 9731 BP; 3021 A; 76 C; 1991 G; 4643 T; 0 U; 0 Other;

Query Match 9.6%; Score 60.2; DB 6; Length 9731;
Best Local Similarity 57.8%; Pred. No. 0.00017;
Matches 107; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 231 TTTTTTTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTT 290
Db 5456 TTATTGTTTTTTTTTTTATTTTATTATTTTGGGAGAAGGGTATTTGGGGGGTAAATAATTT 5515

Qy 291 CAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTG 350
Db 5516 TTTTGTTGTTTGAATTTTTTATATAATTTAAATTTGTGTGTGTGTGTGTGTGTGTGTG 5575

Qy 351 TGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTA 410
Db 5576 TGTGTGTGTGTGTGTATGATAGAGGGAGTTTGTGTGTTAGAGTGTGTTTTTTTTTTTGA 5635

Qy 411 TTTTT 415
Db 5636 TTTTT 5640

RESULT 13
AAS46424
ID AAS46424 standard; DNA; 7135 BP.
XX
AC AAS46424;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #146.
XX
KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-EP002955.
XX
PR 15-MAR-2000; 2000DE-01013847.
PR 06-APR-2000; 2000DE-01019058.
PR 07-APR-2000; 2000DE-01019173.
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumor suppressor
PT genes and oncogenes, useful in designing primers and probes for analyzing
PT diseases associated with cytosine methylation state e.g. cancer.
XX
PS Claim 1; SEQ ID NO 146; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and oncogenes
CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
CC 500 are missing from the sequence listing) sequences (Ss) and sequences
CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
CC probes for detecting the cytosine methylation state and/or single
CC nucleotide polymorphisms and also to be used in an array for analysing
CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
CC probes can also be used in a method for ascertaining genetic and/or
CC epigenetic parameters for the diagnosis and/or therapy of existing
CC diseases or the predisposition to specific diseases, by analysing
CC cytosine methylations. The parameters may be compared to another set of
CC genetic and/or epigenetic parameters, the differences serving as basis
CC for diagnosis and/or prognosis events which are disadvantageous to
CC patients. The present sequence is one of the 533 genomic sequences
CC derived from tumour suppressor genes and oncogenes. Sequences with even
CC numbered Seq ID numbers are the complementary sequence of the
CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
CC 535, except for those whose partner sequence is missing). Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 7135 BP; 2055 A; 118 C; 1901 G; 3061 T; 0 U; 0 Other;

Query Match 8.8%; Score 55.2; DB 4; Length 7135;
Best Local Similarity 56.7%; Pred. No. 0.0027;
Matches 102; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 223 AGGTGGAATTTTTTTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATC 282

```
                ||||| ||| || |    | ||||| | || ||   |||||   |    | | |||| |
Db        426 AGGTGTAATGTTATGAAATGTTTTTATGTTGTAAGTAAAAAGAAGATTTTCGTAAATTTA 485

Qy        283 CCTACTTTCAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTG 342
                |    |       | |||||   |           | | |||  || ||| ||| |||
Db        486 TATTTAATATGTAAAAATATATAATAATTTTTGTATATGATAGAGTTGTGTGTGTGTGTG 545

Qy        343 TGTGTGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTA 402
              |||||||||||| |||||||||||| | | |  | |||     | | || |||||| || |
Db        546 TGTGTGTGTGTGTGTGTGTGTTTTATAAAATAAAAATTTATATTTTGTTTATTATTGA 605


RESULT 14
ABV18162/c
ID   ABV18162 standard; cDNA; 599 BP.
XX
AC   ABV18162;
XX
DT   13-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 18153.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005171.
XX
PR   17-FEB-2000; 2000US-0183319P.
PR   16-MAR-2000; 2000US-0189862P.
PR   25-MAY-2000; 2000US-0207454P.
PR   09-JUN-2000; 2000US-0211314P.
PR   18-JUL-2000; 2000US-0219007P.
PR   13-DEC-2000; 2000US-0255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS   Claim 1; Page 2996; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for: (a) assessing whether
CC   a patient is afflicted with prostate cancer; (b) monitoring the
CC   progression of prostate cancer in a patient; (c) assessing the efficacy
CC   of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC   the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC   determining whether prostate cancer has metastasized in a patient; (h)
CC   assessing the aggressiveness or indolence of prostate cancer in a patient
CC   ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
XX
SQ   Sequence 599 BP; 190 A; 131 C; 124 G; 153 T; 0 U; 1 Other;

  Query Match             8.7%;  Score 54.6;  DB 5;  Length 599;
  Best Local Similarity   68.8%;  Pred. No. 0.0018;
  Matches   75;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy        322 AGAGATGTGCGTGCGTGCGTGTGTGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACA 381
              || |   || ||| ||| ||||||||||||||| |||||||||| | || | || |  ||

Db        344 AGGGCATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAACTGGAAAATGCA 285

Qy        382 GATTTTATTATTTATTTTTTATTTATTTATTTTTTGCAAGTGACTGGCT 430
                | | |   |||||||||| ||| || ||||  |  || | || |||
Db        284 TCTATCTTGTATTATTTTTTTTTTTCTTTTTTTGAGACAGAGCCTTGCT 236


RESULT 15
ABV47950/c
ID   ABV47950 standard; cDNA; 629 BP.
XX
AC   ABV47950;
XX
DT   17-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 47941.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US005171.
XX
PR   17-FEB-2000; 2000US-0183319P.
PR   16-MAR-2000; 2000US-0189862P.
PR   25-MAY-2000; 2000US-0207454P.
PR   09-JUN-2000; 2000US-0211314P.
PR   18-JUL-2000; 2000US-0219007P.
PR   13-DEC-2000; 2000US-0255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS   Claim 1; Page 9416; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for: (a) assessing whether
CC   a patient is afflicted with prostate cancer; (b) monitoring the
CC   progression of prostate cancer in a patient; (c) assessing the efficacy
CC   of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC   the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC   determining whether prostate cancer has metastasized in a patient; (h)
CC   assessing the aggressiveness or indolence of prostate cancer in a patient
CC   ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
XX
SQ   Sequence 629 BP; 202 A; 146 C; 134 G; 147 T; 0 U; 0 Other;

  Query Match             8.7%;  Score 54.6;  DB 5;  Length 629;
  Best Local Similarity   68.8%;  Pred. No. 0.0018;
  Matches   75;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy        322 AGAGATGTGCGTGCGTGCGTGTGTGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACA 381
              || |   || ||| ||| ||||||||||||||| |||||||||| | || | || |  ||

Db        394 AGGGCATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAACTGGAAAATGCA 335

Qy        382 GATTTTATTATTTATTTTTTATTTATTTATTTTTTGCAAGTGACTGGCT 430
                | | |   |||||||||| ||| || ||||  |  || | || |||
Db        334 TCTATCTTGTATTATTTTTTTTTTTCTTTTTTTGAGACAGAGCCTTGCT 286
```

Search completed: April 26, 2005, 16:28:04
Job time : 434.989 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:01:02 ; Search time 3005.16 Seconds
(without alignments)
10125.880 Million cell updates/sec

Title: US-09-601-267-37
Perfect score: 628
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	628	100.0	628	6	BD225834	BD225834 Promoter
2	628	100.0	628	6	AX019583	AX019583 Sequence
3	628	100.0	4044	6	BD225799	BD225799 Promoter
4	628	100.0	4044	6	AX019548	AX019548 Sequence
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6	579	92.2	189715	2	AC121792	AC121792 Mus muscu
7	575.8	91.7	622	6	BD225835	BD225835 Promoter
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11	172	27.4	490	10	AF221922	AF221922 Mus muscu
12	168	26.8	590	10	MMU33831	U33831 Mus musculu
c 13	135.2	21.5	220807	2	AC139643	AC139643 Rattus no
14	89.2	14.2	481	10	AF221916	AF221916 Rattus no
15	79	12.6	397	10	AY058900	AY058900 Mus muscu
16	77.4	12.3	397	10	AY058901	AY058901 Mus spret
17	68.2	10.9	476	10	AF221928	AF221928 Cricetulu
c 18	64	10.2	212070	2	BX897694	BX897694 Danio rer
c 19	62.4	9.9	66375	2	AC100703	AC100703 Mus muscu
c 20	62.4	9.9	117773	10	AL845272	AL845272 Mouse DNA
c 21	62.2	9.9	182881	9	AC090980	AC090980 Homo sapi
c 22	62.2	9.9	183016	2	AC068611	AC068611 Homo sapi
c 23	62.2	9.9	193929	9	AC090797	AC090797 Homo sapi
c 24	62	9.9	163299	2	CR293503	CR293503 Danio rer
c 25	61.4	9.8	247684	2	BX901883	BX901883 Danio rer
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32	59.2	9.4	194734	2	AC083828	AC083828 Homo sapi
33	58.6	9.3	203294	2	CR392349	CR392349 Danio rer
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c 39	57.2	9.1	170027	2	AC110670	AC110670 Canis fam
40	57.2	9.1	209545	2	CR388158	CR388158 Danio rer
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42	57	9.1	154071	3	AC115598	AC115598 Dictyoste
43	57	9.1	163225	9	AC020912	AC020912 Homo sapi
44	57	9.1	198776	5	BX323593	BX323593 Zebrafish
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ALIGNMENTS

RESULT 1
BD225834
LOCUS BD225834 628 bp DNA linear PAT 17-JUL-2003
DEFINITION Promoter region of mouse and human telomerase RNA component genes.
ACCESSION BD225834
VERSION BD225834.1 GI:33035604
KEYWORDS JP 2002509699-A/37.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 628)
AUTHORS Keith,W.N.
TITLE Promoter region of mouse and human telomerase RNA component genes
JOURNAL Patent: JP 2002509699-A 37 02-APR-2002;
CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD
COMMENT OS Mus sp. (mouse)
PN JP 2002509699-A/37
PD 02-APR-2002
PF 29-JAN-1999 JP 2000529424
PR 29-JAN-1998 GB 9801902.9
PI WILLIAM NICOL KEITH
PC
C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K38/00,A61K45/00, PC A61K48/00,
PC A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02 PC ,C12Q1/68//C12N9/12,
PC (A61K35/76,A61K31:522),C12N15/00,A61K37/02,C12N5/00 CC
Promoter region of mouse and human telomerase RNA component CC genes
FH Key Location/Qualifiers
FT source 1. .628
FT /organism='Mus sp. (mouse)'.
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ORIGIN

Query Match 100.0%; Score 628; DB 6; Length 628;
Best Local Similarity 100.0%; Pred. No. 9.1e-168;

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DEFINITION  Sequence 37 from Patent WO9938964.
ACCESSION   AX019583
VERSION     AX019583.1  GI:10043497
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Keith,W.N.
  TITLE     Promoter regions of the mouse and human telomerase rna component
            genes
  JOURNAL   Patent: WO 9938964-A 37 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
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  Query Match           100.0%;  Score 628;  DB 6;  Length 628;
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LOCUS       BD225799                4044 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Promoter region of mouse and human telomerase RNA component genes.
ACCESSION   BD225799
VERSION     BD225799.1  GI:33035569
KEYWORDS    JP 2002509699-A/2.
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4044)
  AUTHORS   Keith,W.N.
  TITLE     Promoter region of mouse and human telomerase RNA component genes
  JOURNAL   Patent: JP 2002509699-A 2 02-APR-2002;
            CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD
COMMENT     OS   Mus sp. (mouse)
            PN   JP 2002509699-A/2
            PD   02-APR-2002
            PF   29-JAN-1999 JP 2000529424
            PR   29-JAN-1998 GB    9801902.9
            PI   WILLIAM NICOL KEITH
            PC
            C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K38/00,A61K45/00, PC
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            PC   A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02 PC
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RESULT 4
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LOCUS       AX019548               4044 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 2 from Patent WO9938964.
ACCESSION   AX019548
VERSION     AX019548.1  GI:10043462
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Keith,W.N.
  TITLE     Promoter regions of the mouse and human telomerase rna component
            genes
  JOURNAL   Patent: WO 9938964-A 2 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 628;  DB 6;  Length 4044;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-167;
  Matches  628;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1610 CGCTGTTTTTCTCGCTGACTTCCAGCGG 1637


RESULT 5
AF047387
LOCUS       AF047387               4044 bp    DNA     linear   ROD 02-APR-1998
DEFINITION  Mus musculus telomerase RNA (terc) gene, promoter and complete
            sequence.
ACCESSION   AF047387
VERSION     AF047387.1  GI:3005556
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4044)
  AUTHORS   Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
            Black,D.M. and Keith,W.N.
  TITLE     Cloning and characterization of human and mouse telomerase RNA gene
            promoter sequences
  JOURNAL   Oncogene 16 (10), 1345-1350 (1998)
  MEDLINE   98206512
   PUBMED   9546436
REFERENCE   2  (bases 1 to 4044)
  AUTHORS   Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
            Black,D.M. and Keith,W.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-1998) Medical Oncology, Beatson Institute,
            Switchback Rd, Glasgow G61 1BD, UK
FEATURES             Location/Qualifiers
     source          1. .4044
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="3"
     gene            1. .1952
                     /gene="terc"
     promoter        1. .1523
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                     /gene="terc"
                     /product="telomerase RNA"
ORIGIN

  Query Match             100.0%;  Score 628;  DB 10;  Length 4044;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-167;
  Matches  628;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 60
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Db       1010 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 1069

Qy         61 GGTCAGCTACCCTTGAAATCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCACT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 GGTCAGCTACCCTTGAAATCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCACT 1129

Qy        121 CACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCGCCACTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1130 CACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCGCCACTT 1189

Qy        181 TTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1190 TTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTTT 1249

Qy        241 TTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1250 TTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAGT 1309

Qy        301 ATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTGTATGTGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1310 ATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTGTATGTGTG 1369

Qy        361 TGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1370 TGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCAA 1429

Qy        421 GTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCCG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1430 GTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCCG 1489

Qy        481 CAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1490 CAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCTA 1549

Qy        541 GGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCC 600
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Db       1550 GGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCC 1609

Qy         601 CGCTGTTTTTCTCGCTGACTTCCAGCGG 628
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Db       1610 CGCTGTTTTTCTCGCTGACTTCCAGCGG 1637


RESULT 6
AC121792
LOCUS       AC121792              189715 bp    DNA     linear   HTG 02-SEP-2004
DEFINITION  Mus musculus chromosome 3 clone RP23-404J7, WORKING DRAFT SEQUENCE,
            21 unordered pieces.
ACCESSION   AC121792
VERSION     AC121792.2  GI:51854627
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 189715)
  AUTHORS   Wilson,R.K.
  TITLE     The sequence of Mus musculus clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 189715)
  AUTHORS   McPherson,J.D. and Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
REFERENCE   3  (bases 1 to 189715)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-SEP-2004) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
COMMENT     On Sep 2, 2004 this sequence version replaced gi:21039881.

            ---------- Genome Center ----------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu
            Contact: submissions@watson.wustl.edu
            ---------- Project Information ----------
            Center project name: M_BA0404J07
            ------------------------------------------------
            ---------- Summary Statistics ----------
            Sequencing vector: M13; 0%
            Sequencing vector: plasmid; 100%
            Chemistry: Dye-primer ET; 0% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 183739 bases at least Q40
            Consensus quality: 184192 bases at least Q30
            Consensus quality: 184706 bases at least Q20
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 21 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1202: contig of 1202 bp in length
            *     1203     1302: gap of unknown length
            *     1303     2621: contig of 1319 bp in length
            *     2622     2721: gap of unknown length
            *     2722     4947: contig of 2226 bp in length
            *     4948     5047: gap of unknown length
            *     5048     6672: contig of 1625 bp in length
            *     6673     6772: gap of unknown length
            *     6773     8697: contig of 1925 bp in length
            *     8698     8797: gap of unknown length
            *     8798    10425: contig of 1628 bp in length
            *    10426    10525: gap of unknown length
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            *    10526    11926: contig of 1401 bp in length
            *    11927    12026: gap of unknown length
            *    12027    13882: contig of 1856 bp in length
            *    13883    13982: gap of unknown length
            *    13983    16240: contig of 2258 bp in length
            *    16241    16340: gap of unknown length
            *    16341    18527: contig of 2187 bp in length
            *    18528    18627: gap of unknown length
            *    18628    21556: contig of 2929 bp in length
            *    21557    21656: gap of unknown length
            *    21657    23825: contig of 2169 bp in length
            *    23826    23925: gap of unknown length
            *    23926    28604: contig of 4679 bp in length
            *    28605    28704: gap of unknown length
            *    28705    32482: contig of 3778 bp in length
            *    32483    32582: gap of unknown length
            *    32583    36528: contig of 3946 bp in length
            *    36529    36628: gap of unknown length
            *    36629    50039: contig of 13411 bp in length
            *    50040    50139: gap of unknown length
            *    50140    59608: contig of 9469 bp in length
            *    59609    59708: gap of unknown length
            *    59709    77103: contig of 17395 bp in length
            *    77104    77203: gap of unknown length
            *    77204   119382: contig of 42179 bp in length
            *   119383   119482: gap of unknown length
            *   119483   152325: contig of 32843 bp in length
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FEATURES             Location/Qualifiers
     source          1. .189715
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="3"
                     /clone="RP23-404J7"
     misc_feature    1. .1202
                     /note="assembly_name:Contig19"
     misc_feature    1303. .2621
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     misc_feature    2722. .4947
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     misc_feature    5048. .6672
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     misc_feature    6773. .8697
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     misc_feature    28705. .32482
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     misc_feature    32583. .36528
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     misc_feature    59709. .77103
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     misc_feature    77204. .119382
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     misc_feature    152426. .189715
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ORIGIN

  Query Match             92.2%;  Score 579;  DB 2;  Length 189715;
  Best Local Similarity   98.4%;  Pred. No. 1.6e-153;
  Matches  619;  Conservative    0;  Mismatches    0;  Indels   10;  Gaps    3;

Qy          1 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 60
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Qy         61 GGTCAGCTACCCTTGAAA-TCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCAC 119
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Db     109419 GGTCAGCTACCCTTGAAATTCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCAC 109478

Qy        120 TCACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCGCCACT 179
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Db     109479 TCACAAGAGATCCGCCTGCCTTCTG----TCAAATTCTGGAATTAAAGATTTGCGCCACT 109534

Qy        180 TTTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTT 239
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Db     109535 TTTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAA-----TTTT 109589

Qy        240 TTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAG 299
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Db     109590 TTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAG 109649

Qy        300 TATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTATGTGT 359
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Db     109650 TATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTATGTGT 109709

Qy        360 GTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCA 419
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Db     109710 GTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCA 109769

Qy        420 AGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCC 479
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Db     109770 AGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCC 109829

Qy        480 GCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCT 539
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Db     109830 GCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCT 109889

Qy        540 AGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGC 599
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Db     109890 AGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGC 109949

Qy        600 CCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
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Db     109950 CCGCTGTTTTTCTCGCTGACTTCCAGCGG 109978


RESULT 7
BD225835
LOCUS       BD225835                622 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Promoter region of mouse and human telomerase RNA component genes.
ACCESSION   BD225835
VERSION     BD225835.1  GI:33035605
KEYWORDS    JP 2002509699-A/38.
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 622)
  AUTHORS   Keith,W.N.
  TITLE     Promoter region of mouse and human telomerase RNA component genes
  JOURNAL   Patent: JP 2002509699-A 38 02-APR-2002;
            CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD
COMMENT     OS   Mus sp. (mouse)
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PN   JP 2002509699-A/38
PD   02-APR-2002
PF   29-JAN-1999 JP 2000529424
PR   29-JAN-1998 GB    9801902.9
PI   WILLIAM NICOL KEITH
PC
C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K38/00,A61K45/00, PC
 A61K48/00,
PC   A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02 PC
,C12Q1/68//C12N9/12,
PC   (A61K35/76,A61K31:522),C12N15/00,A61K37/02,C12N5/00 CC
Promoter region of mouse and human telomerase RNA component  CC
      genes
FH   Key             Location/Qualifiers
FT   source          1. .622
FT                   /organism='Mus sp. (mouse)'.
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 91.7%; Score 575.8; DB 6; Length 622;
Best Local Similarity 98.1%; Pred. No. 6.6e-153;
Matches 617; Conservative 0; Mismatches 2; Indels 10; Gaps 3;

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Qy          1 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 60
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Db          2 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 61

Qy         61 GGTCAGCTACCCTTGAAA-TCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCAC 119
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Db         62 GGTCAGCTACCCTTGAAATTCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCAC 121

Qy        120 TCACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCGCCACT 179
              |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        122 TCACAAGAGATCCGCCTGCCTTCTG----TCAAATTCTGGAATTAAAGATTTGCGCCACT 177

Qy        180 TTTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTT 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 TTTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAA-----TTTT 232

Qy        240 TTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAG 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 TTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAG 292

Qy        300 TATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTGTATGTGT 359
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Db        293 TATATTTCAGAAACCAAGCCTCAGAAATGTGCGTGCGTGCGTGTGTGTGTGTGTATGTGT 352

Qy        360 GTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCA 419
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Db        353 GTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCA 412

Qy        420 AGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCC 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 AGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCC 472

Qy        480 GCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCT 539
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Qy        540 AGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGC 599
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Qy        600 CCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
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RESULT 8

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AX019584
LOCUS       AX019584                622 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 38 from Patent WO9938964.
ACCESSION   AX019584
VERSION     AX019584.1  GI:10043498
KEYWORDS    .
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Keith,W.N.
  TITLE     Promoter regions of the mouse and human telomerase rna component
            genes
  JOURNAL   Patent: WO 9938964-A 38 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES             Location/Qualifiers
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                     /organism="Mus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10095"
ORIGIN
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Query Match 91.7%; Score 575.8; DB 6; Length 622;
Best Local Similarity 98.1%; Pred. No. 6.6e-153;
Matches 617; Conservative 0; Mismatches 2; Indels 10; Gaps 3;

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Qy          1 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 60
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Db          2 TGTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCG 61

Qy         61 GGTCAGCTACCCTTGAAA-TCTTTTTCTTTCTGGAACTCAGTACCTGGTTGGCCATGCAC 119
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Qy        120 TCACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCGCCACT 179
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Qy        180 TTTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTTTTTTT 239
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Qy        240 TTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAACTCTAG 299
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Qy        300 TATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTGTGTGTGTATGTGT 359
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
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Qy        360 GTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTTATTTATTTTTTGCA 419
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Qy        420 AGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCC 479
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Db        413 AGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAAGAGGGAGCATTTCC 472

Qy        480 GCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCT 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 GCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCT 532

Qy        540 AGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGC 599
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        533 AGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTCGTTCTCCGC 592

Qy        600 CCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
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Db        593 CCGCTGTTTTTCTCGCTGACTTCCAGCGG 621
```

RESULT 9

```
AC120377
LOCUS       AC120377              155682 bp    DNA     linear   HTG 13-OCT-2004
DEFINITION  Mus musculus chromosome 3 clone RP24-262L5 map 3, *** SEQUENCING IN
            PROGRESS ***, 4 unordered pieces.
ACCESSION   AC120377
VERSION     AC120377.11  GI:54111356
KEYWORDS    HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 155682)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 3, clone RP24-262L5
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 155682)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
            Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
            Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
            Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAY-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 155682)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
            Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
            Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
            DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
            Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
            Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
            Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
            Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
            Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
            MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
            Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
            Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-OCT-2004) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Oct 13, 2004 this sequence version replaced gi:53374815.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@broad.mit.edu
            -------------- Project Information
                Center project name: L25933
                Center clone name: 262_L_5
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1   110344: contig of 110344 bp in length
            *  110345   110444: gap of unknown length
            *  110445   113121: contig of 2677 bp in length
            *  113122   113221: gap of unknown length
            *  113222   115498: contig of 2277 bp in length
            *  115499   115598: gap of unknown length
            *  115599   155682: contig of 40084 bp in length.
FEATURES             Location/Qualifiers
     source          1. .155682
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="3"
                     /map="3"
                     /clone="RP24-262L5"
                     /clone_lib="RPCI-24 Male Mouse BAC"
ORIGIN

  Query Match             42.0%;  Score 263.6;  DB 2;  Length 155682;
  Best Local Similarity   72.9%;  Pred. No. 1e-63;
  Matches  468;  Conservative    0;  Mismatches  124;  Indels   50;  Gaps    8;

Qy          2 GTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCGG 61
              ||||||||| ||  | ||||||||||||||||| |||||| ||||||||||||||||| |
Db     108651 GTGACCTTGCACGGCTGACCTCCTGCCTCAGCCCCCTACAGGCTGGGATTATAGGCTTGT 108710

Qy         62 GTCAGCTACCCTTGAAA------TCTTTTTCTTTCTGGAACTCAGTA------CCTGGTT 109
              ||||||||||||||||      |||||||||||||||||||| ||      || ||||
Db     108711 GTCAGCTACCCTTGAAATTCTTTCTTTTTCTTTCTGGAACTCAATACATAGGCCAGGTT 108770

Qy        110 GGCC---ATGCACTCACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAA 166
              ||||   ||| |||||||||||||| ||| ||||| |||||||||| |||||| ||||||
Db     108771 GGCCATGATGAACTCACAAGAGATCTGCCAGCCTTTTGTCTCTCAAGTTCTGGGATTAAA 108830

Qy        167 GATTTGCGCCACTTTTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGT 226
              |||||| |||||||                    |  |||||||||||||||||| ||||||
Db     108831 GATTTGTGCCACTT----------------CCCCTGTGGGAGTGGACTGGGTCGAAGGT 108873

Qy        227 GGAATTT-TTTTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGGATTGGAAATATCCCT 285
              ||||||| | |  |||||  |        |    |     ||||| |||| ||||||||||
Db     108874 GGAATTTATGTAGTTTTTAAATGAAAAAGAAAAAGGGTTGGGGGAATTGAAAATATCCCT 108933

Qy        286 ACTTTCAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGT 345
              | |||| ||| || | |||| ||||| |||||  |||||| |||| ||| ||| ||||||
Db     108934 AGTTTCGACTGTAATGTATTCCAGAAGCCAAGTTTCAGAGGTGTGTGTGTGTGTGTGTGT 108993

Qy        346 GTGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTT 405
              ||    ||           |||| |||||||| |||||    | ||| |||    | |||
Db     108994 GTCGCAGT-----------GCTCATAGCAAGAAATAGATTAATTAATTAATTGACTTTTT 109042

Qy        406 ATTTATTTTTTGCAAGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAA 465
              ||  ||| |||||| ||  | |||||| ||||| |||   |||||    || || | |
Db     109043 TATTTATTTATGCAAGAGATGGTCTAGGAGGAGTGAGGAGAAGGGAG----AAGGGAGGA 109098

Qy        466 GAGGGAGCATTTCCGCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAA 525
              | |||| |   || | |||||| |||  ||||||||||||||  ||||||||| |
Db     109099 ATAGCAGCACTAGTGCGAATGCTGGACTCAGCCAATCAGCGCGCGCTGTGGGGTATTAAG 109158

Qy        526 GGTCGAGGGCGGCTAGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGT 585
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                  || |  |||| |   |||||  |   ||||||||| ||| | |||||||||| ||||| |
Db     109159 GGCCACGGGCAGTGTGGCCT--GTGTCTAACCCTGCTTTGCTTTAGCTGTGGATTCTGTT 109216

Qy        586 CTTTTGTTCTCCGCCCGCTGTTTTTCTCGCTGACTTCCAGCG 627
              ||||||| |||||| ||||||||||||||||||||||||| |
Db     109217 CTTTTGTCCTCCGCACGCTGTTTTTCTCGCTGACTTCCAGTG 109258


RESULT 10
AC119995/c
LOCUS       AC119995              179856 bp    DNA     linear   HTG 02-OCT-2004
DEFINITION  Mus musculus chromosome 3 clone RP24-120B18 map 3, *** SEQUENCING
            IN PROGRESS ***, 2 ordered pieces.
ACCESSION   AC119995
VERSION     AC119995.13  GI:53749553
KEYWORDS    HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 179856)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 3, clone RP24-120B18
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 179856)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
            Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
            Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
            Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-MAY-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 179856)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
            Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
            Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
            DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
            Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
            Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
            Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
            Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,
            Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
            MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C.,
            McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
            Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
            O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
            Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
            Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
            Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
            Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-OCT-2004) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Oct 2, 2004 this sequence version replaced gi:51948669.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@broad.mit.edu
            -------------- Project Information
                Center project name: L25880
                Center clone name: 120_B_18
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *       1   162056: contig of 162056 bp in length
            *  162057   162156: gap of unknown length
            *  162157   179856: contig of 17700 bp in length.
FEATURES            Location/Qualifiers
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:10090"
                    /chromosome="3"
                    /map="3"
                    /clone="RP24-120B18"
                    /clone_lib="RPCI-24 Male Mouse BAC"
ORIGIN

  Query Match             42.0%;  Score 263.6;  DB 2;  Length 179856;
  Best Local Similarity   72.9%;  Pred. No. 1.1e-63;
  Matches  468;  Conservative    0;  Mismatches  124;  Indels   50;  Gaps    8;

Qy          2 GTGACCTTGAACTACAGACCTCCTGCCTCAGCCTCCTACAAGCTGGGATTATAGGCTCGG 61
              ||||||||| ||  | |||||||||||||||||| |||||| ||||||||||||||| |
Db     167459 GTGACCTTGCACGGCTGACCTCCTGCCTCAGCCCCCTACAGGCTGGGATTATAGGCTTGT 167400

Qy         62 GTCAGCTACCCTTGAAA------TCTTTTTCTTTCTGGAACTCAGTA------CCTGGTT 109
              |||||||||||||||||      |||||||||||||||||||||| ||      || ||||
Db     167399 GTCAGCTACCCTTGAAATTCTTTTCTTTTTCTTTCTGGAACTCAATACATAGGCCAGGTT 167340

Qy        110 GGCC---ATGCACTCACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAA 166
              ||||   ||| |||||||||||||| ||| ||||| |||||||||| |||||| ||||||
Db     167339 GGCCATGATGAACTCACAAGAGATCTGCCAGCCTTTTGTCTCTCAAGTTCTGGGATTAAA 167280

Qy        167 GATTTGCGCCACTTTTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGT 226
              |||||| ||||||| |                | ||||||||||||||||||| ||||||
Db     167279 GATTTGTGCCACTT----------------CCCCTGTGGGAGTGGACTGGGTCGAAGGT 167237

Qy        227 GGAATTT-TTTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCT 285
              ||||||| | |  |||||  |      |   |     ||||| |||| ||||||||||
Db     167236 GGAATTTATGTAGTTTTTAAATGAAAAAGAAAAAGGGTTGGGGGAATTGAAAATATCCCT 167177

Qy        286 ACTTTCAACTCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGT 345
              | |||| ||| || | |||| ||||| |||||  |||||| |||| ||| ||| ||||||
Db     167176 AGTTTCGACTGTAATGTATTCCAGAAGCCAAGTTTCAGAGGTGTGTGTGTGTGTGTGTGT 167117

Qy        346 GTGTGTGTATGTGTGTGTGTCTCACAGCAAGAAACAGATTTTATTATTTATTTTTTATTT 405
              ||    ||           |||| |||||||| |||||    | ||| |||    | |||
Db     167116 GTCGCAGT----------GCTCATAGCAAGAAATAGATTAATTAATTAATTGACTTTTT 167068

Qy        406 ATTTATTTTTTGCAAGTGACTGGCTAGGAAGAGTGGGGAAGCGGGAGGACAAATGGGGAA 465
              ||  ||| |||||| ||  | |||||| ||||| |||    |||||    || || | |
Db     167067 TATTTATTTATGCAAGAGATGGTCTAGGAGGAGTGAGGAGAAGGGAG----AAGGGAGGA 167012
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Qy        466 GAGGGAGCATTTCCGCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAA 525
              | |||| |   || | |||||| ||| |||||||||||||||  ||||||||| |
Db     167011 ATAGCAGCACTAGTGCGAATGCTGGACTCAGCCAATCAGCGCGCGCTGTGGGGTATTAAG 166952

Qy        526 GGTCGAGGGCGGCTAGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGT 585
              || |  |||| |   |||||  |   ||||||||| ||| | |||||||||| ||||| |
Db     166951 GGCCACGGGCAGTGTGGCCT--GTGTCTAACCCTGCTTTGCTTTAGCTGTGGATTCTGTT 166894

Qy        586 CTTTTGTTCTCCGCCCGCTGTTTTTCTCGCTGACTTCCAGCG 627
              ||||||| |||||| |||||||||||||||||||||||||| |
Db     166893 CTTTTGTCCTCCGCACGCTGTTTTTCTCGCTGACTTCCAGTG 166852


RESULT 11
AF221922
LOCUS       AF221922                490 bp    DNA     linear   ROD 19-MAR-2000
DEFINITION  Mus musculus telomerase RNA gene, sequence.
ACCESSION   AF221922
VERSION     AF221922.1  GI:7263089
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Chen,J.L., Blasco,M.A. and Greider,C.W.
  TITLE     Secondary structure of vertebrate telomerase RNA
  JOURNAL   Cell 100 (5), 503-514 (2000)
  MEDLINE   20185063
   PUBMED   10721988
REFERENCE   2  (bases 1 to 490)
  AUTHORS   Chen,J.-L., Blasco,M.A. and Greider,C.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-2000) Molecular Biology and Genetics, Johns
            Hopkins University School of Medicine, Hunterian 617 / 725 N. Wolfe
            St., Baltimore, MD 21205, USA
FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     CAAT_signal     41. .45
     TATA_signal     63. .68
     misc_RNA        94. .490
                     /product="telomerase RNA"
ORIGIN

  Query Match           27.4%;  Score 172;  DB 10;  Length 490;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-38;
  Matches  172;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        457 AATGGGGAAGAGGGAGCATTTCCGCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGG 516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AATGGGGAAGAGGGAGCATTTCCGCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGG 60

Qy        517 GGTATTTAAGGTCGAGGGCGGCTAGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTG 576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGTATTTAAGGTCGAGGGCGGCTAGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTG 120

Qy        577 GGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 172


RESULT 12
MMU33831
LOCUS       MMU33831                590 bp    DNA     linear   ROD 07-JAN-1998
DEFINITION  Mus musculus telomerase RNA component gene.
ACCESSION   U33831
VERSION     U33831.1  GI:2754700
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 590)
  AUTHORS   Blasco,M.A., Funk,W., Villeponteau,B. and Greider,C.W.
  TITLE     Functional characterization and developmental regulation of mouse
            telomerase RNA
  JOURNAL   Science 269 (5228), 1267-1270 (1995)
  MEDLINE   95381063
   PUBMED   7544492
REFERENCE   2  (bases 1 to 114)
  AUTHORS   Hinkley,C.S., Blasco,M.A., Peng,J., Villeponteau,B., Greider,C.W.
            and Herr,W.
  TITLE     The mouse telomerase RNA 5'end lies just upstream of the telomerase
            template sequence
  JOURNAL   Nucleic Acids Res. (1998) In press
REFERENCE   3  (bases 1 to 590)
  AUTHORS   Blacso,M.A., Funk,W., Villeponteau,B. and Greider,C.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1995) Carol W. Greider, Cold Spring Harbor
            Laboratory, PO Box 100, 1 Bungtown Road, Cold spring Harbor, NY
            11724, USA
REFERENCE   4  (bases 1 to 590)
  AUTHORS   Blacso,M.A., Funk,W., Villeponteau,B. and Greider,C.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-1997) Carol W. Greider, Cold Spring Harbor
            Laboratory, PO Box 100, 1 Bungtown Road, Cold spring Harbor, NY
            11724, USA
  REMARK    Sequence update by submitter
REFERENCE   5  (bases 1 to 590)
  AUTHORS   Blacso,M.A., Funk,W., Villeponteau,B. and Greider,C.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-1998) Carol W. Greider, Cold Spring Harbor
            Laboratory, PO Box 100, 1 Bungtown Road, Cold spring Harbor, NY
            11724, USA
  REMARK    Sequence update by submitter
COMMENT     On Jan 7, 1998 this sequence version replaced gi:2660646.
FEATURES             Location/Qualifiers
     source          1. .590
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /note="initially cloned from D3 embryonic stem cell
                     library"
     CAAT_signal     37. .41
     TATA_signal     59. .65
     snRNA           90. .>483
                     /product="telomerase RNA component"
                     /note="The RNA is approximately 393 nucleotides long. The
                     5' end has been determined, but 3' end has not been
                     precisely mapped. Based on RT-PCR analysis and sequence
                     conservation with the human homolog the 3' end is near
                     position 484 in this sequence"
     misc_feature    90
                     /note="transcription start site"
     misc_feature    92. .99
                     /note="The template region of the RNA specifies the
                     synthesis of the telomere sequence TTAGGG"
ORIGIN

  Query Match           26.8%;  Score 168;  DB 10;  Length 590;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-37;
  Matches  168;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        461 GGGAAGAGGGAGCATTTCCGCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTA 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGAAGAGGGAGCATTTCCGCAAGTGCTGGGCTCGACCAATCAGCGCGCGCCATGGGGTA 60

Qy        521 TTTAAGGTCGAGGGCGGCTAGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTT 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTAAGGTCGAGGGCGGCTAGGCCTCGGCACCTAACCCTGATTTTCATTAGCTGTGGGTT 120

Qy        581 CTGGTCTTTTGTTCTCCGCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 628
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Db        121 CTGGTCTTTTGTTCTCCGCCCGCTGTTTTTCTCGCTGACTTCCAGCGG 168


RESULT 13
AC139643/c
LOCUS       AC139643               220807 bp    DNA     linear   HTG 27-MAR-2003
DEFINITION  Rattus norvegicus clone CH230-208P8, WORKING DRAFT SEQUENCE, 50
            unordered pieces.
ACCESSION   AC139643
VERSION     AC139643.1  GI:28273299
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 220807)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
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            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., Mcleod,M., Mcneill,T., Meenen,E., Milosavljevic,A.,
            Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
            Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,
            Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G.,
            Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
            Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A.,
            Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E.,
            Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,
            Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A.,
            Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S.,
            Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,
            Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E.,
            Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A.,
            Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
            Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D.,
            Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,
            Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R.,
            Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
            Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
            Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
            Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 220807)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-FEB-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 220807)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     -------------- Genome Center
              Center: Baylor College of Medicine
              Center code: BCM
              Web site: http://www.hgsc.bcm.tmc.edu/
              Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
              Center project name: KDRD
              Center clone name: CH230-208P8
            -------------- Summary Statistics
              Sequencing vector: Plasmid;
              Chemistry: Dye-terminator Big Dye: 100% of reads
              Assembly program: Phrap; version 0.990329
              Consensus quality: 184542 bases at least Q40
              Consensus quality: 191076 bases at least Q30
              Consensus quality: 195268 bases at least Q20
              Estimated insert size: 194058; sum-of-contigs estimation
              Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 50 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1572: contig of 1572 bp in length
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            *     1673     3029: contig of 1357 bp in length
            *     3030     3129: gap of unknown length
            *     3130     4854: contig of 1725 bp in length
            *     4855     4954: gap of unknown length
            *     4955     6209: contig of 1255 bp in length
            *     6210     6309: gap of unknown length
            *     6310     7826: contig of 1517 bp in length
            *     7827     7926: gap of unknown length
            *     7927     9049: contig of 1123 bp in length
            *     9050     9149: gap of unknown length
            *     9150    10418: contig of 1269 bp in length
            *    10419    10518: gap of unknown length
            *    10519    12169: contig of 1651 bp in length
            *    12170    12269: gap of unknown length
            *    12270    13764: contig of 1495 bp in length
            *    13765    13864: gap of unknown length
            *    13865    15221: contig of 1357 bp in length
            *    15222    15321: gap of unknown length
            *    15322    16370: contig of 1049 bp in length
            *    16371    16470: gap of unknown length
            *    16471    18058: contig of 1588 bp in length
            *    18059    18158: gap of unknown length
            *    18159    20006: contig of 1848 bp in length
            *    20007    20106: gap of unknown length
            *    20107    21894: contig of 1788 bp in length
            *    21895    21994: gap of unknown length
            *    21995    24019: contig of 2025 bp in length
            *    24020    24119: gap of unknown length
            *    24120    26818: contig of 2699 bp in length
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            *    26919    30012: contig of 3094 bp in length
            *    30013    30112: gap of unknown length
            *    30113    32745: contig of 2633 bp in length
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            *    32846    36746: contig of 3901 bp in length
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            *    36847    39172: contig of 2326 bp in length
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            *    41217    44286: contig of 3070 bp in length
            *    44287    44386: gap of unknown length
            *    44387    46194: contig of 1808 bp in length
            *    46195    46294: gap of unknown length
            *    46295    50409: contig of 4115 bp in length
            *    50410    50509: gap of unknown length
            *    50510    53597: contig of 3088 bp in length
            *    53598    53697: gap of unknown length
            *    53698    59133: contig of 5436 bp in length
            *    59134    59233: gap of unknown length
            *    59234    61999: contig of 2766 bp in length
            *    62000    62099: gap of unknown length
            *    62100    66681: contig of 4582 bp in length
            *    66682    66781: gap of unknown length
            *    66782    70584: contig of 3803 bp in length
            *    70585    70684: gap of unknown length
            *    70685    74052: contig of 3368 bp in length
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  Query Match             21.5%;  Score 135.2;  DB 2;  Length 220807;
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  Matches  257;  Conservative    0;  Mismatches   58;  Indels   37;  Gaps    5;

Qy          2 GTGACCTTGAACTACAGACCTCCTGCCTCAGCC-TCCTACAAGCTGGGATTATAGGCTCG 60
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Db     118727 GTGACCTTGAACTGCTTACCTCCTGCCTCAGCCTTCCTATATGCTGGGATTATAGGCGTG 118668

Qy         61 GGTCAGCTACCCTTGAAATCTTTTTCTTTCTGGAACTCAGT------ACCTGGTTGGCCA 114
              | |||||||||||||    | ||||||||||||||||| ||      |||  ||||||||
Db     118667 TGCCAGCTACCCTTGA---GTCTTTCTTTCTGGAACTCGGTGCATACACCAAGTTGGCCA 118611

Qy        115 TGCACTCACAAGAGATCCGCCTGCCTTCTGTCTCTCAAATTCTGGAATTAAAGATTTGCG 174
              || | | |||| ||||| ||||||||| || |||||||||||||| | ||||||||||||
Db     118610 TGAATTTACAAAAGATCTGCCTGCCTTTTGCCTCTCAAATTCTGGGAGTAAAGATTTGCG 118551

Qy        175 CCACTTTTCCCCACTTCCACCCCCGGCTGTGGGAGTGGACTGGGTTGAAGGTGGAATTTT 234
              |||||           |  |||||||| ||||||||| |||||||| | |||
Db     118550 ACACTT----------------CCCCTGTGGGAATGGACTGGGATGAAGGTGAAGTTTA 118508

Qy        235 TTTTTTTTTTTTTTTTTTTAGTGAAAAAAGGGGGGATTGGAAATATCCCTACTTTCAAC 294
              |||||  ||||   |           || ||||| |||||||| |||| || |||| ||
Db     118507 ATTTTTCTTTTAAAT----------GGAAGGGGGGAATTGGAAAGATCCTTAGTTTCGAC 118458

Qy        295 TCTAGTATATTTCAGAAACCAAGCCTCAGAGATGTGCGTGCGTGCGTGTGTG 346
              |||| | |||||||  || |   |  |||||||||||| | | | | ||||| |
Db     118457 TCTAATGTATTTCATAAGCTGAATCTCAGAGATGTGGGGGGGGGGGTGTGGG 118406


RESULT 14
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LOCUS       AF221916                481 bp    DNA     linear   ROD 19-MAR-2000
DEFINITION  Rattus norvegicus telomerase RNA gene, sequence.
ACCESSION   AF221916
VERSION     AF221916.1  GI:7263083
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 481)
  AUTHORS   Chen,J.L., Blasco,M.A. and Greider,C.W.
  TITLE     Secondary structure of vertebrate telomerase RNA
  JOURNAL   Cell 100 (5), 503-514 (2000)
  MEDLINE   20185063
   PUBMED   10721988
REFERENCE   2  (bases 1 to 481)
  AUTHORS   Chen,J.-L., Blasco,M.A. and Greider,C.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-2000) Molecular Biology and Genetics, Johns
            Hopkins University School of Medicine, Hunterian 617 / 725 N. Wolfe
            St., Baltimore, MD 21205, USA
FEATURES             Location/Qualifiers
     source          1. .481
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ORIGIN

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  Best Local Similarity   82.1%;  Pred. No. 2.3e-14;
  Matches  115;  Conservative    0;  Mismatches   23;  Indels    2;  Gaps    1;

Qy        489 GGGCTCGACCAATCAGCGCGCGCCATGGGGTATTTAAGGTCGAGGGCGGCTAGGCCTCGG 548
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Db         33 GGGCTCAGCCAATCAGCGCGAGCTGTCGGGTATTTAGGGACAAGGGCCGCGCGACTTCTG 92

Qy        549 CACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTT 608
              |  ||||||||  | ||   |||||||||||||| |||||||||||||||||||||||||
Db         93 CGTCTAACCCTATTGTT--ATAGCTGTGGGTTCTGTTCTTTTGTTCTCCGCCCGCTGTTT 150

Qy        609 TTCTCGCTGACTTCCAGCGG 628
              |||||||||||||| ||||||
Db        151 TTCTCGCTGACTTTCAGCGG 170


RESULT 15
AY058900
LOCUS       AY058900                397 bp    DNA     linear   ROD 20-MAR-2002
DEFINITION  Mus musculus castaneus telomerase RNA, genomic sequence.
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ACCESSION   AY058900
VERSION     AY058900.1  GI:16751329
KEYWORDS    .
SOURCE      Mus musculus castaneus (southeastern Asian house mouse)
  ORGANISM  Mus musculus castaneus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 397)
  AUTHORS   Hathcock,K.S., Hemann,M.T., Opperman,K.K., Strong,M.A.,
            Greider,C.W. and Hodes,R.J.
  TITLE     Haploinsufficiency of mTR results in defects in telomere elongation
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (6), 3591-3596 (2002)
   PUBMED   11904421
REFERENCE   2  (bases 1 to 397)
  AUTHORS   Hemann,M.T. and Greider,C.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-OCT-2001) Molecular Biology and Genetics, Johns
            Hopkins University School of Medicine, 725 N. Wolfe St., Hunterian
            617, Baltimore, MD 21205, USA
FEATURES             Location/Qualifiers
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     misc_RNA        1. .397
                     /product="telomerase RNA"
                     /note="untranslated"
ORIGIN

  Query Match             12.6%;  Score 79;  DB 10;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-11;
  Matches   79;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        550 ACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTT 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCTAACCCTGATTTTCATTAGCTGTGGGTTCTGGTCTTTTGTTCTCCGCCCGCTGTTTT 60

Qy        610 TCTCGCTGACTTCCAGCGG 628
              ||||||||||||||||||
Db         61 TCTCGCTGACTTCCAGCGG 79


Search completed: April 26, 2005, 18:27:29
Job time : 3012.16 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 18:27:34 ; Search time 646.625 Seconds
(without alignments)
8140.109 Million cell updates/sec

Title: US-09-601-267-36
Perfect score: 867
Sequence: 1 agctactcaggaggctgaga.....ccctaactgagaagggcgta 867

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	848.6	97.9	2426	9	US-09-057-351-3	Sequence 3, Appli
	2	848.6	97.9	2426	14	US-10-206-447-2	Sequence 2, Appli
	3	848.6	97.9	2426	16	US-10-359-935-3	Sequence 3, Appli
	4	333	38.4	981	10	US-09-895-606-5	Sequence 5, Appli
	5	163	18.8	545	17	US-10-388-360-384	Sequence 384, App
	6	163	18.8	545	18	US-10-831-266-2	Sequence 2, Appli
	7	163	18.8	545	19	US-10-831-267-2	Sequence 2, Appli
	8	110.8	12.8	340449	12	US-09-903-582-3	Sequence 3, Appli
c	9	109.2	12.6	133893	13	US-10-161-510-1	Sequence 1, Appli
c	10	108.8	12.5	201	18	US-10-741-601-25989	Sequence 25989, A
c	11	108.8	12.5	27240	18	US-10-741-601-5777	Sequence 5777, Ap
c	12	108.6	12.5	76698	19	US-10-936-273-30	Sequence 30, Appl
c	13	107.6	12.4	52899	17	US-10-085-117-148	Sequence 148, App
c	14	106.2	12.2	2275	17	US-10-104-047-453	Sequence 453, App
c	15	106.2	12.2	313287	18	US-10-322-281-48	Sequence 48, Appl
c	16	106	12.2	1286	13	US-10-027-632-202645	Sequence 202645,
c	17	106	12.2	1286	17	US-10-027-632-202645	Sequence 202645,
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	41	104	12.0	86361	18	US-10-741-601-5702	Sequence 5702, Ap
	42	104	12.0	86361	19	US-10-741-600-17803	Sequence 17803, A
c	43	103.6	11.9	39451	18	US-10-322-281-554	Sequence 554, App
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	45	103.2	11.9	653122	13	US-10-087-192-226	Sequence 226, App

ALIGNMENTS

RESULT 1
US-09-057-351-3
; Sequence 3, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:

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;      APPLICATION NUMBER:  US 08/472,802
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000821US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-057-351-3

  Query Match            97.9%;  Score 848.6;  DB 9;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 2.5e-253;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

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RESULT 2
US-10-206-447-2
; Sequence 2, Application US/10206447
; Publication No. US20030099616A1
; GENERAL INFORMATION:
;  APPLICANT: Geron Corporation
;  APPLICANT:  Irving, John
;  APPLICANT:  Karpf, David
;  APPLICANT:  Schiff, Michael
;  TITLE OF INVENTION: DUAL SPECIFICITY TUMOR KILLING VECTORS DRIVEN BY THE TELOMERASE P
;  FILE REFERENCE: 085/002
;  CURRENT APPLICATION NUMBER: US/10/206,447
;  CURRENT FILING DATE:  2002-07-25
;  PRIOR APPLICATION NUMBER: 60/308,029
;  PRIOR FILING DATE: 2001-07-25
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 2426
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-206-447-2

  Query Match            97.9%;  Score 848.6;  DB 14;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 2.5e-253;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

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Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
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Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

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Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 3
US-10-359-935-3
; Sequence 3, Application US/10359935
; Publication No. US20030153076A1
;   GENERAL INFORMATION:
;        APPLICANT: Villeponteau, Bryant
;                   Feng, Junli
;                   Funk, Walter
;                   Andrews, William H.
;        TITLE OF INVENTION: Mammalian Telomerase
;        NUMBER OF SEQUENCES: 42
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/359,935
;             FILING DATE: 07-Feb-2003
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/057,351
;             FILING DATE: 08-APR-1994
;             APPLICATION NUMBER: US 08/272,102
;             FILING DATE: 07-JUL-1994
;             APPLICATION NUMBER: US 08/330,123
;             FILING DATE: 27-OCT-1994
;             APPLICATION NUMBER: US 08/472,802
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Storella, John R.
;             REGISTRATION NUMBER: 32,944
;             REFERENCE/DOCKET NUMBER: 015389-000821US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 576-0200
;             TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2426 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-359-935-3

  Query Match             97.9%;  Score 848.6;  DB 16;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 2.5e-253;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

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Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

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Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||
Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 4
US-09-895-606-5
; Sequence 5, Application US/09895606
```

```
; Publication No. US20030207404A1
;  GENERAL INFORMATION:
;       APPLICANT: Villeponteau, Bryant
;                  Feng, Junli
;                  Andrews, William H.
;                  Adams, Robert R.
;       TITLE OF INVENTION: Methods and Reagents for Regulating
;                           Telomere Length and Telomerase Activity
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/895,606
;            FILING DATE: 29-Jun-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/710,249
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: US 60/003,492
;            FILING DATE: 08-SEP-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Storella, John R.
;            REGISTRATION NUMBER: 32,944
;            REFERENCE/DOCKET NUMBER: 015389-001220US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 981 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;            NAME/KEY:  misc_RNA
;            LOCATION:  267..715
;            OTHER INFORMATION:  /product= "hTR"
;            /note= "hTR transcript serves as
;            template in the telomerase
;            ribonucleoprotein"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-895-606-5

  Query Match             38.4%;  Score 333;  DB 10;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 9.9e-93;
  Matches  333;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 CTGCAGAGGATAGAAAAAAGNCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||
Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 5
US-10-388-360-384
; Sequence 384, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
;  APPLICANT: GENOMIC HEALTH
;  APPLICANT:  Baker, Joffre B.
;  APPLICANT:  Cronin, Maureen T.
;  APPLICANT:  Kiefer, Michael C.
;  APPLICANT:  Shak, Steve
;  APPLICANT:  Walker, Michael Graham
;  TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
;  FILE REFERENCE: 39740-0001US
;  CURRENT APPLICATION NUMBER: US/10/388,360
;  CURRENT FILING DATE:  2003-03-12
;  PRIOR APPLICATION NUMBER: US 60/412,049
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: US 60/364,890
;  PRIOR FILING DATE: 2002-03-13
;  NUMBER OF SEQ ID NOS: 384
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 384
;   LENGTH: 545
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-388-360-384

  Query Match             18.8%;  Score 163;  DB 17;  Length 545;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-40;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        705 GAGTGACTCTCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGC 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGTGACTCTCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGC 60

Qy        765 TCCCTTTATAAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGG 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCTTTATAAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGG 120

Qy        825 GGTGGTGGCCATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTGGTGGCCATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 163


RESULT 6
US-10-831-266-2
; Sequence 2, Application US/10831266
; Publication No. US20050003404A1
; GENERAL INFORMATION:
;  APPLICANT: Rowley, Peter T.
;  TITLE OF INVENTION: TELOMERASE INTERFERENCE
;  FILE REFERENCE: A-71506-1/RFT/THR
;  CURRENT APPLICATION NUMBER: US/10/831,266
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: PCT/US 02/33065
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/345,326
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/359,196
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/383,195
;  PRIOR FILING DATE: 2002-05-22
;  NUMBER OF SEQ ID NOS: 17
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;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 545
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-831-266-2

  Query Match             18.8%;  Score 163;  DB 18;  Length 545;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-40;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        705 GAGTGACTCTCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGC 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGTGACTCTCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGC 60

Qy        765 TCCCTTTATAAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGG 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCTTTATAAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGG 120

Qy        825 GGTGGTGGCCATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTGGTGGCCATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 163


RESULT 7
US-10-831-267-2
; Sequence 2, Application US/10831267
; Publication No. US20050009177A1
; GENERAL INFORMATION:
;  APPLICANT: Rowley, Peter T.
;  TITLE OF INVENTION: TELOMERASE INTERFERENCE
;  FILE REFERENCE: A-71506-2/RFT/THR
;  CURRENT APPLICATION NUMBER: US/10/831,267
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: PCT/US 02/33146
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/345,326
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: US 60/359,196
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US 60/383,195
;  PRIOR FILING DATE: 2002-05-22
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 545
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-831-267-2

  Query Match             18.8%;  Score 163;  DB 19;  Length 545;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-40;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        705 GAGTGACTCTCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGC 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGTGACTCTCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGC 60

Qy        765 TCCCTTTATAAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGG 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCTTTATAAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGG 120

Qy        825 GGTGGTGGCCATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTGGTGGCCATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 163


RESULT 8
US-09-903-582-3
; Sequence 3, Application US/09903582
; Publication No. US20050075283A1
; GENERAL INFORMATION:
;  APPLICANT: HU, Song et al.
;  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001274
;  CURRENT APPLICATION NUMBER: US/09/903,582
;  CURRENT FILING DATE:  2001-07-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 340449
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(340449)
;   OTHER INFORMATION: n = A,T,C or G
US-09-903-582-3

  Query Match             12.8%;  Score 110.8;  DB 12;  Length 340449;
  Best Local Similarity   90.8%;  Pred. No. 4.8e-22;
  Matches  118;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||| || |||||||||||||| ||||||||||||||||||||||
Db     249884 AGCTACTCAGGAGGCTGAGGCATGAGAATCGCTTGAATCCGGGAGGCAGAGGTTGCAGTG 249943

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              | | |||||| ||||||| ||||||||||||||||||||| |||| |||||||| ||||
Db     249944 AACTGAGATCGCGCCACTGCACTCCATCCAGCCTGGGCGACAGAGTGAGACTCCGCCTCA 250003

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db     250004 AAAAAAAAAA 250013


RESULT 9
US-10-161-510-1/c
; Sequence 1, Application US/10161510
; Publication No. US20020192695A1
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: PIBs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
;  FILE REFERENCE: EX02-074C
;  CURRENT APPLICATION NUMBER: US/10/161,510
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: US 60/296,076
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/328,605
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/357,253
;  PRIOR FILING DATE: 2002-02-15
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 133893
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-161-510-1

  Query Match             12.6%;  Score 109.2;  DB 13;  Length 133893;
  Best Local Similarity   90.0%;  Pred. No. 9.1e-22;
  Matches  117;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||| |||||||||| || |||||| || ||||||||||||||| ||| |||||||||
Db      63711 AGCTACTCGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGGAGGCGGAGCTTGCAGTG 63652

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||  |||||||||||| |||| || ||||| ||||||||||||
Db      63651 AGCCGAGATCACGCCACTGCACTCCATCCAGCATGGGTGACAGAGCGAGACTCCGTCTCA 63592

Qy        121 AAAAAAAAAA 130
              ||||||||||
```

```
Db      63591 AAAAAAAAAA 63582


RESULT 10
US-10-741-601-25989/c
; Sequence 25989, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25989
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-25989

  Query Match             12.5%;  Score 108.8;  DB 18;  Length 201;
  Best Local Similarity   89.2%;  Pred. No. 3.5e-23;
  Matches  116;  Conservative    1;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||| |||||||||| || |||||| |: ||||||||||||| ||| ||||||||
Db        132 AGCTACTCGGGAGGCTGAGGCAGGAGAATGGSGTGAACCCGGGAGGCGGAGCTTGCAGTG 73

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||||||||||  |||||||||||| |||| || ||||| ||||||||||||
Db         72 AGCCGAGATCACGCCACTGCACTCCATCCAGCATGGGTGACAGAGCGAGACTCCGTCTCA 13

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db         12 AAAAAAAAAA 3


RESULT 11
US-10-741-601-5777/c
; Sequence 5777, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5777
;   LENGTH: 27240
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5777

  Query Match             12.5%;  Score 108.8;  DB 18;  Length 27240;
  Best Local Similarity   89.2%;  Pred. No. 5.1e-22;
  Matches  116;  Conservative    1;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||| |||||||||| || |||||| |: ||||||||||||| ||| ||||||||
Db      11618 AGCTACTCGGGAGGCTGAGGCAGGAGAATGGSGTGAACCCGGGAGGCGGAGCTTGCAGTG 11559

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||||||||||  |||||||||||| |||| || ||||| ||||||||||||
Db      11558 AGCCGAGATCACGCCACTGCACTCCATCCAGCATGGGTGACAGAGCGAGACTCCGTCTCA 11499

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db      11498 AAAAAAAAAA 11489


RESULT 12
US-10-936-273-30/c
; Sequence 30, Application US/10936273
; Publication No. US20050074801A1
; GENERAL INFORMATION:
;  APPLICANT: Monia, Brett P.
;  APPLICANT:  Butler, Madeline M.
;  APPLICANT:  McKay, Robert
;  APPLICANT:  Baker, Brenda F.
;  TITLE OF INVENTION: CHIMERIC OLIGOMERIC COMPOUNDS COMPRISING ALTERNATING REGIONS OF N
;  TITLE OF INVENTION:  AND SOUTHERN CONFORMATIONAL GEOMETRY
;  FILE REFERENCE: ISIS0104-100 (CORE0026US)
;  CURRENT APPLICATION NUMBER: US/10/936,273
;  CURRENT FILING DATE:  2004-09-08
;  NUMBER OF SEQ ID NOS: 221
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 76698
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 15311-15410
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 15414
;   OTHER INFORMATION: n = A,T,C or G
US-10-936-273-30

  Query Match             12.5%;  Score 108.6;  DB 19;  Length 76698;
  Best Local Similarity   81.3%;  Pred. No. 1e-21;
  Matches  126;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||||| || |||||| || ||||||| |||||| ||| |||||||||
Db      15588 AGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCCAGGAGGCGGAGCTTGCAGTG 15529

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||||| ||||||  |||||| |||||||||||||| ||||| |||||| ||||||
Db      15528 AGCCGAGATCATGCCACTGCACTCCAACCAGCCTGGGCGACAGAGCGAGACTCTGTCTCA 15469

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACT 155
              ||||||||||     | ||   | |   || | | |
Db      15468 AAAAAAAAAAAAAAAAAAAAAAGAGGCAGGCTAAGT 15434


RESULT 13
US-10-085-117-148/c
; Sequence 148, Application US/10085117
; Publication No. US20030232334A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: 529452000121
;  CURRENT APPLICATION NUMBER: US/10/085,117
;  CURRENT FILING DATE:  2002-02-27
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 361
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
;   LENGTH: 52899
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: variation
;   LOCATION: (1)...(52899)
;   OTHER INFORMATION: n = any nucleotide
US-10-085-117-148
```

```
  Query Match           12.4%;  Score 107.6;  DB 17;  Length 52899;
  Best Local Similarity  89.2%;  Pred. No. 1.7e-21;
  Matches  116;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||| |||||||||| || |||||| |||||||||||| |||| ||| ||||||||
Db      49315 AGCTACTCGGGAGGCTGAGGCAGGAGAATGGCTTGAACCCGGAAGGCGGAGCTTGCAGTG 49256

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              |||||||||||||||||  |||||||||||||||| || || || |||||| ||||||
Db      49255 AGCCGAGATCACGCCACTGCACTCCATCCAGCCTGGGTGACAGGGCGAGACTCTGTCTCA 49196

Qy        121 AAAAAAAAAA 130
              ||||||||||
Db      49195 AAAAAAAAAA 49186


RESULT 14
US-10-104-047-453/c
; Sequence 453, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20030236392A1el full length cDNA
;  FILE REFERENCE: H1-A0105
;  CURRENT APPLICATION NUMBER: US/10/104,047
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 453
;   LENGTH: 2275
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-104-047-453

  Query Match           12.2%;  Score 106.2;  DB 17;  Length 2275;
  Best Local Similarity  83.9%;  Pred. No. 8.6e-22;
  Matches  120;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||  |||||||||| ||  ||||| |  ||||||| |||||||||| ||||||||
Db       1535 AGCTACTTGGGAGGCTGAGGCAGAAGAATGGTGTGAACCCAGGAGGCAGAGCTTGCAGTG 1476

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||  ||||||  |||||||||||||||||| | ||||||||||||||||||||
Db       1475 AGCCGAGATCGTGCCACTGCACTCCATCCAGCCTGGGCAACAGAGCAAGACTCCGTCTCA 1416

Qy        121 AAAAAAAAAATCGTTACAATTTA 143
              |||  |||  |||  | |  |||| |
Db       1415 AAATAAATAATAATAATAATTAA 1393


RESULT 15
US-10-322-281-48/c
; Sequence 48, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc S. Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: 529452001000
;  CURRENT APPLICATION NUMBER: US/10/322,281
;  CURRENT FILING DATE:  2002-12-17
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 313287
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(313287)
;   OTHER INFORMATION: n = A,T,C or G
US-10-322-281-48

  Query Match           12.2%;  Score 106.2;  DB 18;  Length 313287;
  Best Local Similarity  83.9%;  Pred. No. 1.3e-20;
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Search completed: April 26, 2005, 22:56:08
Job time : 651.625 secs
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 16:02:08 ; Search time 187.318 Seconds
(without alignments)
7573.479 Million cell updates/sec

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Perfect score: 867
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	848.6	97.9	2420	1	US-08-330-123A-3	Sequence 3, Appli
	2	848.6	97.9	2420	3	US-09-580-517-3	Sequence 3, Appli
	3	848.6	97.9	2426	1	US-08-482-115B-3	Sequence 3, Appli
	4	848.6	97.9	2426	2	US-08-660-678A-3	Sequence 3, Appli
	5	848.6	97.9	2426	2	US-08-472-802C-4	Sequence 4, Appli
	6	848.6	97.9	2426	2	US-08-714-482-1	Sequence 1, Appli
	7	848.6	97.9	2426	3	US-08-998-443-3	Sequence 3, Appli
	8	848.6	97.9	2426	3	US-09-060-523-3	Sequence 3, Appli
	9	848.6	97.9	2426	4	US-09-057-351-3	Sequence 3, Appli
	10	834.6	96.3	2425	2	US-08-485-778-1	Sequence 1, Appli
	11	834.6	96.3	2425	3	US-08-520-550A-1	Sequence 1, Appli
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	13	333	38.4	981	2	US-08-710-249-5	Sequence 5, Appli
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ALIGNMENTS

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US-08-330-123A-3
; Sequence 3, Application US/08330123A
; Patent No. 5583016
;  GENERAL INFORMATION:
;    APPLICANT:  VILLEPONTEAU, Bryant
;    APPLICANT:  FENG, Junli
;    APPLICANT:  FUNK, Walter
;    APPLICANT:  ANDREWS, William H.
;    TITLE OF INVENTION:  HUMAN TELOMERASE
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/330,123A
;      FILING DATE:  27-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15389-000810
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2420 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-330-123A-3

  Query Match            97.9%;  Score 848.6;  DB 1;  Length 2420;
  Best Local Similarity  99.4%;  Pred. No. 1.6e-274;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;
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RESULT 2
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; Sequence 3, Application US/09580517
; Patent No. 6320039
;   GENERAL INFORMATION:
;        APPLICANT: VILLEPONTEAU, Bryant
;                   FENG, Junli
;                   FUNK, Walter
;                   ANDREWS, William H.
;        TITLE OF INVENTION: HUMAN TELOMERASE
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend Khourie and Crew
;             STREET: 379 Lytton Avenue
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: US
;             ZIP: 94301
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/580,517
;             FILING DATE: 25-May-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/330,123
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Smith, William M
;             REGISTRATION NUMBER: 30,223
;             REFERENCE/DOCKET NUMBER: 15389-000810
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 326-2400
;             TELEFAX: (415) 326-2422
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2420 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-580-517-3

  Query Match             97.9%;  Score 848.6;  DB 3;  Length 2420;
  Best Local Similarity   99.4%;  Pred. No. 1.6e-274;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;
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RESULT 3
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; Sequence 3, Application US/08482115B
; Patent No. 5776679
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Assays for the RNA Component of Human
;    TITLE OF INVENTION:  Telomerase
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,115B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000830US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-482-115B-3

  Query Match             97.9%;  Score 848.6;  DB 1;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 1.6e-274;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

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Qy        421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
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Db       1081 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 4
US-08-660-678A-3
; Sequence 3, Application US/08660678A
; Patent No. 5837857
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;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/660,678A
;      FILING DATE:  05-JUN-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000811US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-660-678A-3

  Query Match             97.9%;  Score 848.6;  DB 2;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 1.6e-274;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
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Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
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Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
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Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||
Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 5
US-08-472-802C-4
; Sequence 4, Application US/08472802C
; Patent No. 5958680
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,802C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15389-000820
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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-472-802C-4

  Query Match             97.9%;  Score 848.6;  DB 2;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 1.6e-274;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
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Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
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Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
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Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||
Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 6
US-08-714-482-1
; Sequence 1, Application US/08714482
; Patent No. 5972605
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Harley, Calvin
;    TITLE OF INVENTION:  Assays for Regulators of Mammalian
;    TITLE OF INVENTION:  Telomerase Expression
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/714,482
;      FILING DATE:  16-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/521,634
;      FILING DATE:  31-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/482,115
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/472,802
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-00860US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..2426
;      OTHER INFORMATION:  /note= "SauIIIA1-HindIII fragment
;      OTHER INFORMATION:  containing hTR sequences as well as
;      OTHER INFORMATION:  transcription regulatory sequences"
US-08-714-482-1

  Query Match             97.9%;  Score 848.6;  DB 2;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 1.6e-274;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
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Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
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Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
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Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 7
US-08-998-443-3
; Sequence 3, Application US/08998443
; Patent No. 6054575
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,443
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/660,678
;      FILING DATE:  05-JUN-1996
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000811US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-998-443-3

  Query Match             97.9%;  Score 848.6;  DB 3;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 1.6e-274;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140
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Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||
Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527
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RESULT 8
US-09-060-523-3
; Sequence 3, Application US/09060523
; Patent No. 6258535
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/060,523
;      FILING DATE:  14-APR-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/660,678
;      FILING DATE:  05-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000813US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-060-523-3

  Query Match             97.9%;  Score 848.6;  DB 3;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 1.6e-274;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
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Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
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Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||
Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527
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RESULT 9
US-09-057-351-3
; Sequence 3, Application US/09057351
; Patent No. 6548298
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/057,351
;      FILING DATE:  08-APR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/472,802
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000821US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-057-351-3

  Query Match             97.9%;  Score 848.6;  DB 4;  Length 2426;
  Best Local Similarity   99.4%;  Pred. No. 1.6e-274;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
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Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
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Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
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Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy        841 TGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||
Db       1501 TGTCTAACCCTAACTGAGAAGGGCGTA 1527


RESULT 10
US-08-485-778-1
; Sequence 1, Application US/08485778
; Patent No. 5876979
;  GENERAL INFORMATION:
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Avilion, Ariel Athena
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Greider, Carol
;    APPLICANT:  Marhuenda, Maria Antonia Blasco
;    APPLICANT:  Villeponteau, Bryant
;    TITLE OF INVENTION:  RNA COMPONENT OF TELOMERASE
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,778
;      FILING DATE:  07-JE-1995
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;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/387,524
;       FILING DATE:  13-FEB-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/330,123
;       FILING DATE:  27-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/272,102
;       FILING DATE:  07-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Granahan, Patricia
;       REGISTRATION NUMBER:  32,227
;       REFERENCE/DOCKET NUMBER:  CSHL94-05A4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-861-6240
;       TELEFAX:  617-861-9540
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2425 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-485-778-1

  Query Match             96.3%;  Score 834.6;  DB 2;  Length 2425;
  Best Local Similarity   99.0%;  Pred. No. 8.5e-270;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    5;  Gaps    2;

Qy          1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
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Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
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Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGC----GGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 836
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Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 1500

Qy        837 TTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db       1501 TTTTTGTCTAACCCTAACTGAGAAGGGCGTA 1531


RESULT 11
US-08-520-550A-1
; Sequence 1, Application US/08520550A
; Patent No. 6013468
;  GENERAL INFORMATION:
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Avilion, Ariel A.
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Greider, Carol
;    APPLICANT:  Marhuenda, Maria A. B.
;    APPLICANT:  Villeponteau, Bryant
;    TITLE OF INVENTION:  RNA Component of Telomerase
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/520,550A
;      FILING DATE:  29-AUG-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/387,524
;      FILING DATE:  13-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  CSHL94-05A3B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2425 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-520-550A-1
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  Best Local Similarity  99.0%;  Pred. No. 8.5e-270;
  Matches  862;  Conservative    0;  Mismatches    4;  Indels    5;  Gaps    2;

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Db        662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy         61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
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Db        721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy        121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy        181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy        241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy        301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
              |||||| |||||||||||||||||| || |||||||||| |||||||||||||||||||
Db        961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy        361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy        421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
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Db       1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy        481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
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Db       1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy        541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
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Db       1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy        601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
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Db       1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy        661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
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Db       1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy        721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
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Db       1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy        781 CTCGCCCGGCAGCGCACCGGGTTGC----GGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 836
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Db       1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 1500

Qy        837 TTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||
Db       1501 TTTTTGTCTAACCCTAACTGAGAAGGGCGTA 1531


RESULT 12
US-08-714-482-2
; Sequence 2, Application US/08714482
; Patent No. 5972605
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Harley, Calvin
;    TITLE OF INVENTION:  Assays for Regulators of Mammalian
;    TITLE OF INVENTION:  Telomerase Expression
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/714,482
;      FILING DATE:  16-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/521,634
;      FILING DATE:  31-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/482,115
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/472,802
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-00860US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  981 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..981
;      OTHER INFORMATION:  /note= "PstI fragment containing hTR
;      OTHER INFORMATION:  sequence"
US-08-714-482-2

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  Best Local Similarity  100.0%;  Pred. No. 1.3e-101;
  Matches  334;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
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Db          1 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
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Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
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Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240
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Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
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Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 13
US-08-710-249-5
; Sequence 5, Application US/08710249
; Patent No. 5858777
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Adams, Robert R.
;    TITLE OF INVENTION:  Methods and Reagents for Regulating
;    TITLE OF INVENTION:  Telomere Length and Telomerase Activity
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/710,249
;      FILING DATE:  13-SEP-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/583,808
;      FILING DATE:  05-JAN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/003,492
;      FILING DATE:  08-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001220US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  981 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  267..715
;      OTHER INFORMATION:  /product= "hTR"
;      OTHER INFORMATION:  /note= "hTR transcript serves as
;      OTHER INFORMATION:  template in the telomerase
;      OTHER INFORMATION:  ribonucleoprotein"
US-08-710-249-5

  Query Match             38.4%;  Score 333;  DB 2;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 2.8e-101;
  Matches  333;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
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Db          1 CTGCAGAGGATAGAAAAAAGNCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
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Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
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Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
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Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
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Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
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Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 14
US-09-220-157A-5
; Sequence 5, Application US/09220157A
; Patent No. 6300110
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Adams, Robert R.
;    TITLE OF INVENTION:  Methods and Reagents for Regulating
;    TITLE OF INVENTION:  Telomere Length and Telomerase Activity
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/220,157A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/710,249
;      FILING DATE:  13-SEP-1996
;      APPLICATION NUMBER:  US 08/583,808
;      FILING DATE:  05-JAN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/003,492
;      FILING DATE:  08-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001220US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  981 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
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;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  267..715
;      OTHER INFORMATION:  /product= "hTR"
;      OTHER INFORMATION:  /note= "hTR transcript serves as
;      OTHER INFORMATION:  template in the telomerase
;      OTHER INFORMATION:  ribonucleoprotein"
US-09-220-157A-5

  Query Match            38.4%;  Score 333;  DB 3;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 2.8e-101;
  Matches  333;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
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Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
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Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
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Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||
Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


RESULT 15
US-08-770-565-1
; Sequence 1, Application US/08770565
; Patent No. 5846723
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Nam Woo
;    APPLICANT:  Wu, Fred
;    APPLICANT:  Kealey, James T.
;    APPLICANT:  Pruzan, Ronald
;    APPLICANT:  Weinrich, Scott L.
;    TITLE OF INVENTION:  Methods for Detecting the RNA Component of
;    TITLE OF INVENTION:  Telomerase
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/770,565
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-002300US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  981 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-770-565-1

  Query Match            38.3%;  Score 332.4;  DB 2;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 4.4e-101;
  Matches  333;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
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Db          1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
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Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 867
              |||||||||||||||||||||||||||||||||
Db        301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTA 334


Search completed: April 26, 2005, 20:19:01
Job time : 192.318 secs
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